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100897

From: Sullivan, Daniel
Sent: Tuesday, August 12, 2003 8:23 AM
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Mail Box: 11E12
Tel: 703-305-4448

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Phone: _____
Location: _____
Date Picked Up: 8/13
Date Completed: 8/21
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

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AA Sequences: _____
Structures: _____
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Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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PA (HYBR-) HYBRIGENICS.
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 PI Legrain P, Benarous R, Blot G, Lassot I;
 XX
 XX WPI: 2002-508795/54.
 DR P-PSDB; MAU98087.
 XX
 XX Protein-protein complexes for screening drugs or agents that modulate
 PT interaction of proteins, e.g. for identifying the Selected Interacting
 PT Domains (SID), comprises interaction between beta-Trcp and Ras Sfl -
 XX
 XX Claim 2: Page 46-47; 84pp: English.
 PS
 XX The present invention relates to a new complex of protein-protein
 CC interaction between betaTrcp (not defined in specification) and Ras Sfl.
 CC The protein-protein complex of the invention is useful for screening
 CC drugs or agents that modulate interaction of proteins. In particular,
 CC the protein complex is useful for identifying the Selected Interacting
 CC Domains (SID). The modulating compounds detected can be used for
 CC treating tumours. The polynucleotides encoding the protein complex may
 CC be used in gene therapy. The present nucleic acid sequence encodes the
 CC human beta Trcp (bTrcp) protein that was used in the methods of the
 CC invention as a bait protein.
 CC
 XX Sequence 657 BP: 211 A; 131 C; 163 G; 152 T; 0 other:
 SO
 Query Match 100.0%; Score 657; DB 24; Length 657;
 Best Local Similarity 100.0%; Pred. No. 1.1e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACCCGGCGGCGGTCTGTCAGAGAGAGACGCTCAAGTTATGATTCCTCAGAG 60
 DB 1 ATGGACCCGGCGGCGGTCTGTCAGAGAGAGACGCTCAAGTTATGATTCCTCAGAG 60
 QY 61 AGAAGAGACTGTAATATGCGGAACCCCTAGAGATATACAGAGAAATTCACCTT 120
 DB 61 AGAAGAGACTGTAATATGCGGAACCCCTAGAGATATACAGAGAAATTCACCTT 120
 QY 121 AGACAGACATCAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGATGTTTACGA 180
 DB 121 AGACAGACATCAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGATGTTTACGA 180
 QY 181 AGCACTGCTATGAGAGACTGAGAAATTTGTGGCCAAACAACTTGGCAATGGCACTTCC 240
 DB 181 AGCACTGCTATGAGAGACTGAGAAATTTGTGGCCAAACAACTTGGCAATGGCACTTCC 240
 QY 241 AGATGATGTGGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAGAAAGAACTG 300
 DB 241 AGATGATGTGGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAGAAAGAACTG 300
 QY 301 TGTGTCAAAATCTTTGAGCACTGTGTCAGAGTCAAGTGAATTTGTGGAACATCTT 360
 DB 301 TGTGTCAAAATCTTTGAGCACTGTGTCAGAGTCAAGTGAATTTGTGGAACATCTT 360
 QY 361 ATATCCCAATGTGTCTATTACCAATGGGCATATAAATCTGTATCTTAAACCTATGTG 420
 DB 361 ATATCCCAATGTGTCTATTACCAATGGGCATATAAATCTGTATCTTAAACCTATGTG 420
 QY 421 CAGAGAGATTCATTAACCTGCTCTGCAAGCTGGGGATTGATCATATGCGTGAACACTT 480
 DB 421 CAGAGAGATTCATTAACCTGCTCTGCAAGCTGGGGATTGATCATATGCGTGAACACTT 480
 QY 481 CTGTCTATACCTGTGATGCGCAATCACTATGTGCTCTGCAACTTGTGTGCAAGATGTGAC 540
 DB 481 CTGTCTATACCTGTGATGCGCAATCACTATGTGCTCTGCAACTTGTGTGCAAGATGTGAC 540
 QY 541 CGAGTACCTGTGATGCGATCTGTGGAAGAAGCTTATCGAGAGATGTGTCAGACAGAT 600
 DB 541 CGAGTACCTGTGATGCGATCTGTGGAAGAAGCTTATCGAGAGATGTGTCAGACAGAT 600
 QY 601 TCCTGTGGAGAGGCGTGGCAGAACGAAGGATGGGAGCATTTATTTAATCAAAAC 657
 DB 601 TCCTGTGGAGAGGCGTGGCAGAACGAAGGATGGGAGCATTTATTTAATCAAAAC 657

DB 601 TCCTGTGGAGAGGCGTGGCAGAACGAAGGATGGGAGCATTTATTTAATCAAAAC 657
 RESULT 2
 AAA73132
 ID AAA73132 standard; cDNA: 1707 BP.
 XX
 XX AAA73132;
 AC
 AC 27-NOV-2000 (first entry)
 DT
 XX Human beta-transducin repeat containing protein (beta-Trcp) cDNA.
 DE
 XX Ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikappab;
 KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FBD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-Trcp; ss.
 XX
 OS Homo sapiens.
 PN JP2000166542-A.
 PD 20-JUN-2000.
 XX
 XX 02-DEC-1998; 98JP-0343437.
 XX
 XX 02-DEC-1998; 98JP-0343437.
 XX
 XX (KAGA-) KAGANU GIJUNSU SHINKO JIGYODAN.
 PA WPI: 2000-485550/43.
 DR P-PSDB; AAB12813.
 XX
 XX F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of Ikappab or beta-catenin -
 PT
 XX Disclosure: Fig 17; 19pp; Japanese.
 PS
 CC The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of Ikappab or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and WD40
 CC repeat motif and has the amino acid sequence of 43 residues (AAB12813)
 CC or one of two 366 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FBD1 protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-Trcp)). The F-box protein can be used for
 CC the gene therapy of colon cancer by being recombined to a virus vector.
 CC The present sequence encodes the human beta-Trcp protein from the
 CC present invention.
 CC
 XX Sequence 1707 BP: 514 A; 349 C; 414 G; 430 T; 0 other;
 SO
 Query Match 100.0%; Score 657; DB 21; Length 1707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCCGGCGGCGGTCTGTCAGAGAGAGACGCTCAAGTTATGATTCCTCAGAG 60
 DB 1 ATGGACCCGGCGGCGGTCTGTCAGAGAGAGACGCTCAAGTTATGATTCCTCAGAG 60
 QY 61 AGAAGAGACTGTAATATGCGGAACCCCTAGAGATATACAGAGAAATTCACCTT 120
 DB 61 AGAAGAGACTGTAATATGCGGAACCCCTAGAGATATACAGAGAAATTCACCTT 120
 QY 121 AGACAGACATCAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGATGTTTACGA 180
 DB 121 AGACAGACATCAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGATGTTTACGA 180
 QY 181 AGCACTGCTATGAGAGACTGAGAAATTTGTGGCCAAACAACTTGGCAATGGCACTTCC 240
 DB 181 AGCACTGCTATGAGAGACTGAGAAATTTGTGGCCAAACAACTTGGCAATGGCACTTCC 240
 QY 241 AGATGATGTGGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAGAAAGAACTG 300
 DB 241 AGATGATGTGGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAGAAAGAACTG 300

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Db 241 ACTATGATTGCCCCAGCAACGAACTCTCAGACAGTATGAAAGGAAAGCAACTG 300
Oy 301 TGTGCAAACTACTTGTAGCAGTGTGAGATGATGATGATGATGATGATGATGATGAT 360
Db 301 TGTGCAAACTACTTGTAGCAGTGTGAGATGATGATGATGATGATGATGATGATGAT 360
Oy 361 ATATCCCAAAATGTGATTTACCAACATGAGGACATTAATCTGATTTAAACCTATGTTG 420
Db 361 ATATCCCAAAATGTGATTTACCAACATGAGGACATTAATCTGATTTAAACCTATGTTG 420
Oy 421 CAGAGAGATTTGATTAAGTCTGCTGCGACAGTGTGAGATGATGATGATGATGATGATGAT 480
Db 421 CAGAGAGATTTGATTAAGTCTGCTGCGACAGTGTGAGATGATGATGATGATGATGATGAT 480
Oy 481 CTGTCTATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 CTGTCTATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Oy 541 CGAGTGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 CGAGTGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Oy 601 TCTCTGTGAGAGGCTGCGACAGCAAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 657
Db 601 TCTCTGTGAGAGGCTGCGACAGCAAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 657

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RESULT 3

AAx86501
ID AAX86501 standard; cDNA; 2151 BP.

AAx86501;

20-MAR-2003 (updated)
30-SEP-1999 (first entry)

DE cDNA encoding a human beta-transducin repeat containing protein.

XX Beta-transducin repeat containing protein; beta-Trcp; Skrip;
XX proteosome degradation pathway; Vpu protein; beta-catenin;
XX human immune deficiency virus-1; HIV-1; cellular protein; IKKpab;
XX ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;
XX antiviral; antitumour; cell cycle regulation; protein degradation;
XX and anti-inflammatory; osteo-articular inflammation; acute inflammation;
XX tumour necrosis factor; ss.

OS Homo sapiens.

PH Location/Qualifiers
FT CDS 70..1779

FT /product= beta-Trcp
FT /note= "beta-transducin repeat containing protein"

PN W0938969-A1.

XX 05-AUG-1999.

XX 29-JAN-1999; 99WO-PR00196.

XX 09-DEC-1998; 98FR-0015545.

XX 30-JAN-1998; 98FR-0001100.

XX (INSP) INST PASTEUR.

XX (INRM) INST NAT SANTE & RECH MEDICALE.

XX Arenzana Seisdedos F, Benarous R, Concordet J, Durand H;

XX Kroll M, Margotlin F;

XX WPI: 1999-469329/39.

XX DR P-PSDB; AAY24054.

```

PT New human beta-transducin repeat containing protein and its
PT fragments useful as, or to screen for, antiviral, antitumour,
PI anti-inflammatory and anti-Alzheimer's agents
PS Claim 7: Page 57-60; 71pp: French.
XX
XX The present sequence encodes a human beta-transducin repeat containing
CC protein (beta-Trcp). The protein directs proteins to the proteosome
CC degradation pathways. The protein is able to interact with the Vpu
CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins
CC Ikappab or beta-catenin (bc) and/or protein Skrip. The protein controls
CC ubiquitinylation of phosphorylated proteins and thus their targeting to
CC proteosomes for degradation. Depending on whether the process is
CC inhibited or promoted, the result may be delayed breakdown of Cdk4 (in
CC cases of HIV-1 infection); increased activity of Ikb (and thus reduced
CC activity of NFkappab); increased degradation of mutant bc in tumour
CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
CC patients. The beta-Trcp protein, and its active peptide fragments, or its
CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
CC antitumour agents that disrupt cell cycle regulation or protein
CC degradation in human tumour cells, and anti-inflammatory agents that
CC disrupt activation by NFkappab. Fragments of the protein are also
CC useful for treating osteo-articular inflammation or acute inflammation
CC associated with release of tumour necrosis factor.
CC (Updated on 20-MAR-2003 to correct PA field.)
XX
SQ Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

```

Query Match 100.0%; Score 657; DB 20; Length 2151;

Best local similarity 100.0%; Pred. No. 2,1e-201;

Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 ATGACCCGCGGCGGAGCGGTGCTGCAAGAGAGCACTCAAGTTTATGATTCCTCAGAG 60
Db 70 ATGACCCGCGGCGGAGCGGTGCTGCAAGAGAGCACTCAAGTTTATGATTCCTCAGAG 129
Oy 61 AGAGAACTGTATATATATGCGGCAACCCCTAGAGATATATACAGAGAAATTCACATT 120
Db 130 AGAGAACTGTATATATGCGGCAACCCCTAGAGATATATACAGAGAAATTCACATT 189
Oy 121 AGACAGACATPACAAACGCTGTGCGACAGCTGTTTAAACCAAGAAACATATGTTAGCA 180
Db 190 AGACAGACATPACAAACGCTGTGCGACAGCTGTTTAAACCAAGAAACATATGTTAGCA 249
Oy 181 AGCACTGCTATGAGAACTGAGATTTGTGTGCGCAAAACAACTTCCATGAGCACTTCC 240
Db 250 AGCACTGCTATGAGAACTGAGATTTGTGTGCGCAAAACAACTTCCATGAGCACTTCC 309
Oy 241 AGTATGATTTGTGCGGCAAGCAAGGAAACTCTCAGCAAGCTATGAAAAAGAAAGAACTG 300
Db 310 AGTATGATTTGTGCGGCAAGCAAGGAAACTCTCAGCAAGCTATGAAAAAGAAAGAACTG 369
Oy 301 TGTGCAAACTACTTGTAGCAGTGTGAGATGATGATGATGATGATGATGATGATGATGAT 360
Db 370 TGTGCAAACTACTTGTAGCAGTGTGAGATGATGATGATGATGATGATGATGATGATGAT 429
Oy 361 ATATCCCAATGTGTCATTTACCAACATGAGGACATTAATCTGATTTAAACCTATGTTG 420
Db 430 ATATCCCAATGTGTCATTTACCAACATGAGGACATTAATCTGATTTAAACCTATGTTG 489
Oy 421 CAGAGAGATTTGATTAAGTCTGCTGCGACAGTGTGAGATGATGATGATGATGATGATGAT 480
Db 490 CAGAGAGATTTGATTAAGTCTGCTGCGACAGTGTGAGATGATGATGATGATGATGATGAT 549
Oy 481 CTGTCTATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 550 CTGTCTATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
Oy 541 CGAGTGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 610 CGAGTGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
Oy 601 TCTCTGTGAGAGGCTGCGACAGCAAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAT 657

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|||||
DB 670 TCCTGTGGAGAGGCGCTGGCAGAACGAGAGGATGGGAGCTATTATTTCACAAAC 726
RESULT 4
ID AAA51229 standard; DNA: 2151 BP.
XX
AC AAA51229:
XX
DT 26-SEP-2000 (first entry)
XX
DE Human beta-TTCP coding sequence.
XX
KM E3 ubiquitin ligase; beta-TTCP; F-box; WD protein; I-kappa-B; inhibitor;
KM nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KM anti-inflammatory; immunosuppressive; cytostatic; ds.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 70..1779
FT /*tag= a
FT /product= Human_TTCP
XX
PN MO200034447-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US29371.
XX
PR 10-DEC-1998; 98US-0210060.
XX
PA (SIGN-) SIGNAL PHARM INC.
PA (YISS) YISSUM RES & DEV CO.
PI Manning AM, Mercurio F, Amlt S, Ben-eriah Y, Davis M, Hatzubai A;
PI Layon I, Yaron A;
XX
DR WPI: 2000-431294/37.
DR P-PSDB: NAY96697.
XX
PT Polypeptide enhancing phosphorylated Ikkappa ubiquitination useful for
PT treating disorder associated with NF-kappa activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
PT variant
XX
PS Disclosure; Page 72; 77pp; English.
XX
CC This DNA encodes human beta-TTCP, an F-box/WD protein family member,
CC which has been shown to have homology to human E3 ubiquitin ligase (E3).
CC E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor
CC of protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
CC degradation via the ubiquitin pathway is useful for identifying
CC modulators of this process for use in treating diseases associated with
CC activation of NF-kappa-B. In vitro analysis suggests that deletion of
CC the F-box results in a protein that functions as a dominant negative
CC molecule in vivo. Transient over-expression of delta-beta-TTCP (a
CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha
CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated
CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
CC activity. E3 and beta-TTCP can be used to modulate NF-kappa-B to treat
CC inflammatory diseases, autoimmune diseases, cancer and viral infections.
XX
SO Sequence 2151 BP: 628 A; 467 C; 513 G; 543 T; 0 other;
Query Match 100.0%; Score 657; DB 21; Length 2151;
Best Local Similarity 100.0%; Pred. No. 2.1e-201;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCCCGGCGGCGGCTGCGAAGAGAGGACATCAAGTTTATGATTCTCTCAGAG 60
DB 70 ATGAGCCCGGCGGCGGCTGCGAAGAGAGGACATCAAGTTTATGATTCTCTCAGAG 129

QY 61 AGAGAGACTGTATTAATGGCGAACCCCTAGGAAGATTAATCCAGAGACATTCACCTT 120
DB 130 AGAGAGACTGTATTAATGGCGAACCCCTAGGAAGATTAATCCAGAGACATTCACCTT 189
QY 121 AGACAGACATCAACAGCTGTGCCAGACTGTGCTTAATCAACGAAGAGATGTTTACCA 180
DB 190 AGACAGACATCAACAGCTGTGCCAGACTGTGCTTAATCAACGAAGAGATGTTTACCA 249
QY 181 AGACAGCTGTATGAAGACTGAGAAATGTGTGGCCAAACAACTTGCATGGCCTTCC 240
DB 250 AGCACTGCTATGAAGACTGAGAAATGTGTGGCCAAACAACTTGCATGGCCTTCC 309
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DB 310 AGTATGATTTGGCCCAAGCAACGGAACCTTCAGCAGCTTATGAAGAGAAAGCACTG 369
QY 301 TGTGTCAAATACCTTTGAGCAGTGGGCAAGTCAGATCAAGTGAATTTGTGAACATCTT 360
DB 370 TGTGTCAAATACCTTTGAGCAGTGGGCAAGTCAGATCAAGTGAATTTGTGAACATCTT 429
QY 361 ATATCCCAATATGTGTATTTACCAACATGGGACATTAACCTGTATTTAACTATGTTG 420
DB 430 ATATCCCAATATGTGTATTTACCAACATGGGACATTAACCTGTATTTAACTATGTTG 489
QY 421 CAGAGAGATTTCAATACCTGCTCCAGCTCGGGGATTTGATCATATGCTGAGAACATT 480
DB 490 CAGAGAGATTTCAATACCTGCTCCAGCTCGGGGATTTGATCATATGCTGAGAACATT 549
QY 481 CTGTCAATACCTGATGCGCAATCACTATGCTCTGCAACTGTGTGCAAGAAATGTGAC 540
DB 550 CTGTCAATACCTGATGCGCAATCACTATGCTCTGCAACTGTGTGCAAGAAATGTGAC 609
QY 541 CGAGTGAACCTGTGATGGCATCTGTGGAAGAAGCTTATCGAGAGATGTCAGACAGAT 600
DB 610 CGAGTGAACCTGTGATGGCATCTGTGGAAGAAGCTTATCGAGAGATGTCAGACAGAT 669
QY 601 TCCTGTGGAGAGGCGCTGGCAGAACGAGAGATGGGACAGTATTATTTCACAAAC 657
DB 670 TCCTGTGGAGAGGCGCTGGCAGAACGAGAGATGGGACAGTATTATTTCACAAAC 726
RESULT 5
ID AAZ93350
ID AAZ93350 standard; cDNA: 2151 BP.
XX
AC AAZ93350:
XX
DT 16-AUG-2000 (first entry)
XX
DE Sequence encoding F-box protein FBP-1.
XX
KM F-box protein; FBP; diagnosis; treatment; screening; agonist;
KM antagonist; proliferative disorder; differential disorder;
KM breast cancer; prostate cancer; ovarian cancer; cancer;
KM small cell lung carcinoma; immune disorder; cardiovascular disorder;
KM inflammatory disorder; human; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 70..1779
FT /*tag= a
FT /product= FBP-1
XX
PN WO200012679-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-US19560.
XX
PR 28-AUG-1998; 98US-0098355.
PR 03-FEB-1999; 99US-0118568.

PR 15-MAR-1999: 99US-0124449.
 XX (UWNY) UNITV NEW YORK STATE.
 PA Chlaure DS, Pagano M, Latres E;
 PI MPI: 2000-256635/22.
 XX F-PSDB: AA183041.
 DR Novel nucleic acid for screening compounds useful for treating
 XX proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases
 PS Disclousure; Figure 3b, 3c, 3d; 245pp; English.
 XX Nucleic acids encoding substrate-targeting subunits of ubiquitin
 CC ligases with F-box motifs (F-box proteins) are useful for diagnosis
 CC of proliferative and differentiated related disorders by measuring
 CC FBP gene expression. Cells expressing such proteins or
 CC their fragments are useful for screening compounds. The compounds
 CC are agonists or antagonists, which are useful for treating a
 CC proliferative or differentiative disorder in a mammal such as
 CC breast, ovarian and prostate cancer and small cell lung carcinoma
 CC and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein,
 CC analogs, derivatives and their subsequences, anti-FBP antibodies,
 CC are also useful in diagnosis of the disorders.

Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

Query Match 100.0%; Score 657; DB 21; Length 2151;
 Best Local Similarity 100.0%; Pred. No. 2.1e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGACCCGGGCGAGGCGGTGCGAAGAGGCGACCAAGTTTGAATTCCTCAGAG 60
 DB 70 ATGGACCCGGGCGAGGCGGTGCTGCAGAGAGGCGCTCAAGTTTGAATTCCTCAGAG 129
 OY 61 AGAGAACTGTAAATATGCGCAACCCCTAGGAGATATACAGAGAGAAATTCACAT 120
 DB 130 AGAGAACTGTAAATATGCGCAACCCCTAGGAGATATACAGAGAGAAATTCACAT 189
 OY 121 AGAGAGACTATACAGAGCTGTGCGAGACTCTGCTTAACCAAGAAACAGTATGTTAGCA 180
 DB 190 AGAGAGACTATACAGAGCTGTGCGAGACTCTGCTTAACCAAGAAACAGTATGTTAGCA 249
 OY 181 AGACACTGTATGAGAGCTGAGAAATGTGTGGCCAAAGAAACCTGCCAATGGCACTTCC 240
 DB 250 AGACACTGTATGAGAGCTGAGAAATGTGTGGCCAAAGAAACCTGCCAATGGCACTTCC 309
 OY 241 AGATGATATGTGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAAGAAAGAACTG 300
 DB 310 AGATGATATGTGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAAGAAAGAACTG 369
 OY 301 TGTGTCAATTAATCTTGGAGAGTGTGAGTCAAGTCAAGTGAATTTGTGAAACATCTT 360
 DB 370 TGTGTCAATTAATCTTGGAGAGTGTGAGTCAAGTCAAGTGAATTTGTGAAACATCTT 429
 OY 361 AATATCCCAATGTCATTAACCAACATGGGCAATGAATTCGATTTAACTTAAGTTG 420
 DB 430 AATATCCCAATGTCATTAACCAACATGGGCAATGAATTCGATTTAACTTAAGTTG 489
 OY 421 CAGAGAGATTTTCAATTAATCTCTGCCAGCTCGGGGATTTGGATCAATTCCTCGAGACAT 480
 DB 490 CAGAGAGATTTTCAATTAATCTCTGCCAGCTCGGGGATTTGGATCAATTCCTCGAGACAT 549
 OY 481 CTGTCTATACCTGATGAGCCCAATCACTATGTCTGCTGAACCTGTGTGCAAGAGATGAC 540
 DB 550 CTGTCTATACCTGATGAGCCCAATCACTATGTCTGCTGAACCTGTGTGCAAGAGATGAC 609
 OY 541 CGAGTGACCTGTGATGAGCCGTCGTCGAGAGAGCTTATGAGAGATGTCGAGACAGAT 600
 DB 610 CGAGTGACCTGTGATGAGCCGTCGTCGAGAGAGCTTATGAGAGATGTCGAGACAGAT 669

OY 601 TCTCTGTGAGAGCCCTGGCAGAACGAGAGATGGGACAGTATTATTCATAAAC 657
 DB 670 TCTCTGTGAGAGCCCTGGCAGAACGAGAGATGGGACAGTATTATTCATAAAC 726
 RESULT 6
 ID AA293710
 XX AA293710 standard; DNA; 2151 BP.
 AC AA293710;
 XX 16-AUG-2000 (first entry)
 DE F-box protein hbetaTrcP coding sequence.
 XX
 KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..179
 FT /tag= a
 FT /product= F-box protein hbetaTrcP
 XX
 PN W0200022110-A2.
 XX
 PD 20-APR-2000.
 XX
 PD 08-OCT-1999; 99WO-US23705.
 XX
 PF 09-OCT-1998; 98US-0103787.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Zhou P, Howley P;
 XX
 DR MPI: 2000-317970/27.
 XX
 P-PSDB: AA183250.
 XX

Targeting degradation of polypeptide useful for treating cancer and
 other proliferative disorders, involves conjugating polypeptide with
 PT ubiquitin protein ligase or inhibiting ubiquitination using organic
 PT compound

Claim 10; Page 171; 185pp; English.

XX The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.

Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

Query Match 100.0%; Score 657; DB 21; Length 2151;
 Best Local Similarity 100.0%; Pred. No. 2.1e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID ALA1041 standard; cDNA; 2151 BP.
 AC ALA1041;
 XX
 XX
 DT 11-OCT-2002 (first entry)
 DE
 XX cDNA of Human F-box protein FBP1 SEQ ID No 1.
 DE
 KW Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial;
 KW differentiative; differentiative disorder; Skp2; F-box protein; cancer;
 KW ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
 KW small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
 KW inflammatory disorder; lymphoma; major opportunistic infection;
 KW certain cardiovascular disease; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200255665-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 07-JAN-2002; 2002MO-US00311.
 XX
 PR 05-JAN-2001; 2001US-260179P.
 XX
 PA (UYNV) UNIV NEW YORK STATE.
 XX
 PI Pagano M;
 XX
 DR WPI: 2002-599665/64.
 DR P-PSDB: AAO22446.
 XX
 PT Screening compounds for treating proliferative disorders, e.g. breast
 PT cancer or prostate cancer. Infections or immune disorders, comprises
 PT detecting a change in the activity of Skp2 with either p27 or Cks1 -
 XX
 PS Disclosure: Fig 3; 246pp; English.
 XX
 XX The invention relates to screening compounds useful for the treatment of
 CC proliferative or differentiative disorders comprising detecting a change
 CC in the activity of Skp2 (F-box protein). The method is useful for
 CC screening compounds for the treatment of proliferative or differentiative
 CC disorders, particularly cancer. These compounds include small molecules,
 CC or compounds or derivatives or analogues of the new ubiquitin ligases.
 CC The compounds are useful for treating diseases such as cancer (e.g.
 CC breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
 CC lung carcinoma or parathyroid adenomas), major opportunistic infections,
 CC immune disorders, certain cardiovascular diseases or inflammatory
 CC disorders. This polynucleotide sequence represents the cDNA encoding an
 CC F-box protein (FBP) of the invention.
 XX
 SO Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

Query Match 100.0%; Score 657; DB 24; Length 2151;
 Best Local Similarity 100.0%; Pred. No. 2.1e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCGGCGGCGGCTGTCGACAGAGACGACGATTTATGATTCCTCAGAG 60
 DB 70 ATGGACCGCGGCGGCGGCTGTCGACAGAGAGGACGACGATTTATGATTCCTCAGAG 129
 QY 61 AGAGAAAGCTTAATATGCGAACCCCTAGAGATATACAGAGAAAGATTCACATT 120
 DB 130 AGAGAAAGCTTAATATGCGAACCCCTAGAGATATACAGAGAAAGATTCACATT 189
 QY 121 AGACAGACATACACAGCTGTGCGACGACTGCTTAAACAGAGAAAGATTCACATT 180
 DB 190 AGACAGACATACACAGCTGTGCGACGACTGCTTAAACAGAGAAAGATTCACATT 249
 QY 181 AGACAGCTATGAGAGACTGAGAAATGTGTGGCCAAAGAAACCTTCCAAATGGCACTTCC 240
 DB 230 AGACAGCTATGAGAGACTGAGAAATGTGTGGCCAAAGAAACCTTCCAAATGGCACTTCC 309

QY 241 AGTATGATTGTGCCCAACGCAACGGAAGAACTCTCAGCAAGCTATGAAAGAAAGAAAGCACTG 300
 DB 310 AGTATGATTGTGCCCAACGCAACGGAAGAACTCTCAGCAAGCTATGAAAGAAAGAAAGCACTG 369
 QY 301 TGTGTCAAAATACCTTTGAGCAGTGTGTCAGAGTCAGATCAGATGGAATTTGTGGAACTCTT 360
 DB 370 TGTGTCAAAATACCTTTGAGCAGTGTGTCAGAGTCAGATCAGATGGAATTTGTGGAACTCTT 429
 QY 361 ATATCCCAAAATGTCATTTACCAACATGCGCAATAACTGATCTTAAACCTATGTG 420
 DB 430 ATATCCCAAAATGTCATTTACCAACATGCGCAATAACTGATCTTAAACCTATGTG 489
 QY 421 CAGAGAGATTTCAATACCTGCTCTGCGACCTGCGGAGATTTGATCATATGCTGAGAACATT 480
 DB 490 CAGAGAGATTTCAATACCTGCTCTGCGACCTGCGGAGATTTGATCATATGCTGAGAACATT 549
 QY 481 CTGTCTATACCTTGATGCGATGCGTGTGGAAGAACTTATCGAGAGAAATGTGACGACAT 540
 DB 550 CTGTCTATACCTTGATGCGATGCGTGTGGAAGAACTTATCGAGAGAAATGTGACGACAT 609
 QY 541 CGAGTACCTCTGATGCGATGCGTGTGGAAGAACTTATCGAGAGAAATGTGACGACAT 600
 DB 610 CGAGTACCTCTGATGCGATGCGTGTGGAAGAACTTATCGAGAGAAATGTGACGACAT 669
 QY 601 TCTCTGTGTGAGAGGCTGCGAGAAACGAGAGATGGGACATATTATTCAAAAC 657
 DB 670 TCTCTGTGTGAGAGGCTGCGAGAAACGAGAGATGGGACATATTATTCAAAAC 726

RESULT 9
 ABS51009
 ID ABS51009 standard; cDNA; 2151 BP.
 XX
 AC ABS51009;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human cDNA encoding bait protein beta-TrCP1.
 XX
 KW Human; ss; gene; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
 KW non-insulin diabetes mellitus; obesity; selected interacting domain;
 KW SID; protein-protein interaction map; PWM; anorectic; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200253726-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 28-DEC-2001; 2001MO-EP15423.
 XX
 PR 02-JAN-2001; 2001US-259377P.
 XX
 PA (HYBR-) HYBRIGENICS.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Legrain P, Marullo S, Jockers R;
 XX
 DR WPI: 2002-583612/62.
 DR P-PSDB: ABG69473.
 XX
 PT Novel complex of protein-protein interactions in adipocyte cells for
 PT identifying compounds that modulate the protein-protein interactions
 PT and useful for treating obesity and metabolic disorders -
 XX
 PS Claim 2; Page -: 125pp; English.
 XX
 CC The invention relates to a complex of protein-protein interactions
 CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
 CC defined in the specification, or polynucleotides in adipocytes encoding
 CC for the polypeptides. Also included are a recombinant cell expressing the
 CC interacting polypeptides and a method of selecting a modulating compound
 CC in adipocyte cells, by cultivating a recombinant host cell on a selective

CC medium containing a modulating compound and a reporter gene the
 CC expression of which is toxic for the recombinant host cell which is
 CC transformed with two vectors, where the first vector comprises a
 CC polynucleotide encoding a first hybrid polypeptide and DNA binding
 CC domain and the second vector comprising a polynucleotide encoding a
 CC second hybrid polypeptide and an activating domain that activates the
 CC toxic reporter gene, when the first and second hybrid polypeptides
 CC interact and selecting the modulating compound which inhibits the
 CC growth of the recombinant host cell (i.e. using the yeast two-hybrid
 CC system). The complexes are useful for identifying compounds that modulate
 CC the protein-protein interactions and useful for treating obesity and
 CC metabolic disorders e.g. non-insulin dependent diabetes mellitus,
 CC NIDDM. The compound isolated by the method is useful for treating and
 CC preventing obesity or metabolic diseases. The interactions between
 CC the proteins of the complex further define a set of selected interacting
 CC domains, SID. The present sequence encodes a member of the protein
 CC complex of the invention, used as the bait protein in the yeast two-
 CC hybrid assay.
 CC Note: The present sequence was not displayed in the specification but
 CC was obtained from its Genbank entry by the indexer.
 CC
 XX

Sequence 2151 BP: 628 A: 467 C: 513 G: 543 T: 0 other;

Query Match 100.0%; Score 657; DB 24; Length 2151;

Best Local Similarity 100.0%; Pred. No. 2,1e-201; Mismatches 0; Indels 0; Gaps 0;

DB 1 ATGAGACCCGGCGGCGGCTGCTGCAAGAGAGGACTCAAGTTATGAAATTCCTCAGAG 60
 70 ATGAGACCCGGCGGCGGCTGCTGCAAGAGAGGACTCAAGTTATGAAATTCCTCAGAG 129
 QY 61 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCTT 120
 DB 130 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCTT 189
 QY 121 AGACAGACATACACAGCTGTGCGAGACTGCTTAAACCAAGAAAGATGTTTGGCA 180
 DB 190 AGACAGACATACACAGCTGTGCGAGACTGCTTAAACCAAGAAAGATGTTTGGCA 249
 QY 181 AGCACTGCTATGAAAGACTGAGAAATGTGTGCCAAAACAAACTTGGCAATGGCACTTCC 240
 DB 250 AGCACTGCTATGAAAGACTGAGAAATGTGTGCCAAAACAAACTTGGCAATGGCACTTCC 309
 QY 241 AGTATGATTTGTGCCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAGAAAGAACTGTG 300
 DB 310 AGTATGATTTGTGCCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAGAAAGAACTGTG 369
 QY 301 TGTGTCAAAATCTTTGAGCAAGTGTGAGAGTCAAGTCAAGTATTTGTTGAACATCTT 360
 DB 370 TGTGTCAAAATCTTTGAGCAAGTGTGAGAGTCAAGTCAAGTATTTGTTGAACATCTT 429
 QY 361 ATATCCCAATGTGTCTATTACCAACATGGGCACATTAATCTGTAAACCTATGTTG 420
 DB 430 ATATCCCAATGTGTCTATTACCAACATGGGCACATTAATCTGTAAACCTATGTTG 489
 QY 421 CAGAGAGATTTCAATTAATGCTGTGCGCAAGCTCGGGGATTTGATCATTCGCTGAGAAATTT 480
 DB 490 CAGAGAGATTTCAATTAATGCTGTGCGCAAGCTCGGGGATTTGATCATTCGCTGAGAAATTT 549
 QY 481 CTGTCAATACCTGTGATGCGCAATCACTATGTCTGCTGAATCTGTGTCAAGAAATGCTTAC 540
 DB 550 CTGTCAATACCTGTGATGCGCAATCACTATGTCTGCTGAATCTGTGTCAAGAAATGCTTAC 609
 QY 541 CGAGTGAACCTGTGATGCGCAATCACTATGTCTGCTGAATCTGTGTCAAGAAATGCTTAC 600
 DB 610 CGAGTGAACCTGTGATGCGCAATCACTATGTCTGCTGAATCTGTGTCAAGAAATGCTTAC 669
 QY 601 TCTCTGTGAGAGGCGCTGCGAGAAAGAGAGATGGGAGACAGATTTATTCATAAAAC 657
 DB 670 TCTCTGTGAGAGGCGCTGCGAGAAAGAGAGATGGGAGACAGATTTATTCATAAAAC 726

RESULT 10

AA229233
 ID AA229233 standard; cDNA; 2419 BP.
 AC AA229233;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Human cell signalling protein-12 encoding cDNA.
 XX
 KW Cell signalling protein-12; CSIGP-12; cell proliferation;
 KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
 KW arteriosclerosis; Addison's disease; multiple sclerosis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..1779
 FT /tag=a
 FT /product="Cell Signalling Protein-12"
 FT
 XX
 PN WO958558-A2.
 XX
 PD 18-NOV-1999.
 XX
 PE 13-MAY-1999; 99WO-US10567.
 XX
 PR 13-MAY-1998; 98US-0085343.
 XX
 PR 26-AUG-1998; 98US-0098010.
 XX
 PA (INCYTE) INCYTE PHARM INC.
 XX
 PI Bandman O, Hillman JL, Lal P, Yue H, Tang, YT, Patterson C;
 PI Baughn MR, Yang J;
 XX
 DR WPI: 2000-086432/07.
 DR P-PSDB: AAY44249.
 XX
 PT Human cell signalling proteins useful for, e.g. diagnosing cell
 PT proliferative and inflammatory disorders
 PS
 PS Claim 9; Page 87-88; 90pp; English.
 CC
 CC The present sequence is a cDNA obtained from Incyte clone 3239149 of
 CC COLAUCT01 library. It encodes cell signalling protein-12 (CSIGP-12). It
 CC is expressed in musculo-skeletal, gastrointestinal and nervous
 CC tissues. Fragments of CSIGP encoding nucleic acid can be used as
 CC hybridisation probe for detecting CSIGP related sequences or allelic
 CC variants. Recombinant CSIGP can be produced in host cells by transforming
 CC them with genetically engineered vectors. Agonists or antagonists can be
 CC used in the treatment of cell proliferative and inflammatory disorders
 CC associated with decreased or increased CSIGP expression. CSIGP is used in
 CC the diagnosis, prevention and treatment of cell proliferative disorders
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 CC
 XX
 SO Sequence 2419 BP: 671 A: 531 C: 625 G: 590 T: 2 other;

Query Match 99.8%; Score 655.4; DB 21; Length 2419;
 Best Local Similarity 99.8%; Pred. No. 7.3e-201;
 Matches 656; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGACCCGGCGGCGGCTGCTGCAAGAGAGGACTCAAGTTATGAAATTCCTCAGAG 60
 DB 70 ATGAGACCCGGCGGCGGCTGCTGCAAGAGAGGACTCAAGTTATGAAATTCCTCAGAG 129
 QY 61 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCTT 120
 DB 130 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCTT 189
 QY 121 AGACAGACATACACAGCTGTGCGAGACTGCTTAAACCAAGAAAGATGTTTGGCA 180
 DB 190 AGACAGACATACACAGCTGTGCGAGACTGCTTAAACCAAGAAAGATGTTTGGCA 249

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OY 181 AGCACTGCTATGAGAGACTGAGAAATTTGTGTGCCCCAAAACAACTTCCCATGCGACTTCC 240
    |||||||
DB 250 AGCACTGCTATGAGAACTGAGAAATTTGTGTGCCCCAAAACAACTTCCCATGCGACTTCC 309
OY 241 AGTATGATTTGTGCCCAAGCAACGGAACCTCAGCAAGCTATGAAAGAAAGGAAGACTG 300
    |||||||
DB 310 AGTATGATTTGTGCCCAAGCAACGGAACCTCAGCAAGCTATGAAAGAAAGGAAGACTG 369
OY 301 TGTGTCAAAATCTTTGAGCAGTGTGTCAGAGTCAGATCAAGTGAATTTGTGGAAACATCTT 360
    |||||||
DB 370 TGTGTCAAAATCTTTGAGCAGTGTGTCAGAGTCAGATCAAGTGAATTTGTGGAAACATCTT 429
OY 361 ATATCCCAAAATGTGTCAATTTACCAACATGGGCATATAAATCTGTATCTTAACCTATGTG 420
    |||||||
DB 430 ATATCCCAAAATGTGTCAATTTACCAACATGGGCATATAAATCTGTATCTTAACCTATGTG 489
OY 421 CAGAGAGATTTCAATACCTGCTGCTGCGAGTGGGATTTGATTCATATGCTGAGAACAT 480
    |||||||
DB 490 CAGAGAGATTTCAATACCTGCTGCTGCGAGTGGGATTTGATTCATATGCTGAGAACAT 549
OY 481 CTGTCTATACCTGGAGTCCCAATCACTATGTGCTGCAACTTTGTGCAAGGAATGTATC 540
    |||||||
DB 550 CTGTCTATACCTGGAGTCCCAATCACTATGTGCTGCAACTTTGTGCAAGGAATGTATC 609
OY 541 CGAGTGACCTCTGATGCGATGCTGTGGAAGAACTTATCGAGAGATGTGTCAGACAGAT 600
    |||||||
DB 610 CGAGTGACCTCTGATGCGATGCTGTGGAAGAACTTATCGAGAGATGTGTCAGACAGAT 669
OY 601 TCTCTGTGGAGAGGCTGTGGCAAGAGAGAGATGGGAGATTTATTTCAAAAAC 657
    |||||||
DB 670 TCTCTGTGGAGAGGCTGTGGCAAGAGAGAGATGGGAGATTTATTTCAAAAAC 726

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RESULT 11

AAH90079 ID AAH90079 standard; cDNA; 3220 BP.

AAH90079;

01-OCT-2001 (first entry)

Human bone marrow cDNA, SEQ ID NO: 323.

Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;

antiviral; antibacterial; antifungal; anti-HIV; haemostatic;

immunosuppressive; gene therapy; cytokine cell proliferation;

cell differentiation modulator; immune disorder; infection; cancer;

human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.

Homo sapiens.

WO200153453-A2.

26-JUL-2001.

23-DEC-2000; 2000WO-US34960.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

30-NOV-2000; 2000US-0250583.

(HYSE-) HYSEQ INC.

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DR P-PSDB: AAM0960.
XX
XX Novel bone-marrow-expressed polynucleotides and polypeptides, useful
PT for treating e.g. cancer and immune deficiency disorders -
XX
XX Claim 1; Page 428; 648pp; English.
XX
XX The present sequence is one of 251 novel human polynucleotides
CC expressed in the bone marrow. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various
CC immune deficiencies and disorders. The deficiencies and disorders may
CC be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous
CC system disorder such as Alzheimer's disease. Detection of the presence
CC or increased expression of the polynucleotide or the protein it
CC encodes is useful for the diagnosis and/or prognosis of one
CC or more types of cancer. The polynucleotide and polypeptide can be
CC used as nutritional sources or supplements and in the screening of
CC chemical compounds as potential drugs.
XX
XX Sequence 3220 BP; 878 A; 725 C; 770 G; 847 T; 0 other;

```

Query Match 99.3%; Score 652.2; DB 22; Length 3220;
Best Local Similarity 99.5%; Pred. No. 9, 1e-200;
Matches 654; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 ATGGACCCCGCCGAGCGGTGCTGCAAGAGAGCGCATTTATGATTCCTCAGAG 60
    |||||||
DB 128 ATGGACCCCGGTGAGCGGTGCTGCAAGAGAGCGCATTTATGATTCCTCAGAG 187
OY 61 AGAGAAAGACTGTAATATGCGCAACCCCTAGAGATTAATACAGAGAAATTCAT 120
    |||||||
DB 188 AGAGAAAGACTGTAATATGCGCAACCCCTAGAGATTAATACAGAGAAATTCAT 247
OY 121 AGACAGACATACACAGCTGTGCGCAGACTGTCTTAACCAAGAAACAGTATGTTAGCA 180
    |||||||
DB 248 AGACAGACATACACAGCTGTGCGCAGACTGTCTTAACCAAGAAACAGTATGTTAGCA 307
OY 181 AGCACTGCTATGAGAGAGTGTGTTGGCCAAACAACTTGCCAAATGGCACTTCC 240
    |||||||
DB 308 AGCACTGCTATGAGAGAGTGTGTTGGCCAAACAACTTGCCAAATGGCACTTCC 367
OY 241 AGTATGATTTGTGCCCAAGCAACGGAACCTCAGCAAGCTATGAAAGAAAGGAAGACTG 300
    |||||||
DB 368 AGTATGATTTGTGCCCAAGCAACGGAACCTCAGCAAGCTATGAAAGAAAGGAAGACTG 427
OY 301 TGTGTCAAAATCTTTGAGCAGTGTGTCAGAGTCAGATCAAGTGAATTTGTGGAACATCTT 360
    |||||||
DB 428 TGTGTCAAAATCTTTGAGCAGTGTGTCAGAGTCAGATCAAGTGAATTTGTGGAACATCTT 487
OY 361 ATATCCCAAAATGTGTCAATTTACCAACATGGGCATATAAATCTGTATCTTAACCTATGTG 420
    |||||||
DB 488 ATATCCCAAAATGTGTCAATTTACCAACATGGGCATATAAATCTGTATCTTAACCTATGTG 547
OY 421 CAGAGAGATTTCAATACCTGCTGCTGCGAGTGGGATTTGATTCATATGCTGAGAACAT 480
    |||||||
DB 548 CAGAGAGATTTCAATACCTGCTGCTGCGAGTGGGATTTGATTCATATGCTGAGAACAT 607
OY 481 CTGTCTATACCTGGAGTCCCAATCACTATGTGCTGTGAACCTTGTCAGAGGAATGTATC 540
    |||||||
DB 608 CTGTCTATACCTGGAGTCCCAATCACTATGTGCTGTGAACCTTGTCAGAGGAATGTATC 667
OY 541 CGAGTGACCTCTGATGCGATGCTGTGGAAGAACTTATCGAGAGATGTGTCAGACAGAT 600
    |||||||
DB 668 CGAGTGACCTCTGATGCGATGCTGTGGAAGAACTTATCGAGAGATGTGTCAGACAGAT 727
OY 601 TCTCTGTGGAGAGGCTGTGCAAGAGAGAGATGGGAGATTTATTTCAAAAAC 657
    |||||||
DB 728 TCTCTGTGGAGAGGCTGTGCAAGAGAGAGATGGGAGATTTATTTCAAAAAC 784

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WPI: 2001-488707/53.

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RESULT 12
AKS1715
ID AAKS1715 standard; cDNA; 2285 BP.
XX
XX AAKS1715;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 260.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Dimanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX P-PSDB: AAM78582.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 1177-1180; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activating/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 2285 BP; 646 A; 492 C; 573 G; 574 T; 0 other;
XX
XX Query Match 92.9%; Score 610.2; DB 22; Length 2285;
XX Best Local Similarity 99.5%; Pred. No. 2.9e-186;
XX Matches 612; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 43 TTTATGAATTCCTAGAGAGAGAGAGACTGTAATATGCGCAACCCCTAGGAATATA 102
XX TTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX 277 TTGATGAATTCCTAGAGAGAGAGAGACTGTAATATGCGCAACCCCTAGGAATATA 336
XX
XX 103 CCAGAGAGAAATTCATTAGACAGATACAAAGCTGTGCGACAGACTGCTTAACCAA 162
XX
XX
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DB 337 CCAGAGAGAAATTCCTAGACAGACATACAAAGCTGTGCCAGACTGCTTAACCAA 396
OY 163 GAAACAGATATGTTAGCAAGCAGCTGTATGAAGACTGAAATTTGTGGCAAAACAAA 222
DB 397 GAAACAGATATGTTAGCAAGCAGCTGTATGAAGACTGAAATTTGTGGCAAAACAAA 456
OY 223 CTTGCCAATGCGACTTCCAGTATGATTTGTGCCCAAGCAAGAACTCTAGCAAGCTAT 282
DB 457 CTTGCCAATGCGACTTCCAGTATGATTTGTGCCCAAGCAAGAACTCTAGCAAGCTAT 516
OY 283 GAAAGAGAAAGAAAGAACTGTGTCAAAATCTTTAGACAGCTGTGAGATCAATCAAGTG 342
DB 517 GAAAGAGAAAGAAAGAACTGTGTCAAAATCTTTAGACAGCTGTGAGATCAATCAAGTG 576
OY 343 GAATTTGTGGAACATCTTATATCCCAATGTGTCAATACCAATGAGGACATATACTCG 402
DB 577 GAATTTGTGGAACATCTTATATCCCAATGTGTCAATACCAATGAGGACATATACTCG 636
OY 403 TATCTTAAACCTATGTTGACAGAGAGATTTCATTAACCTGCTGCCAGCTGGGGATTGGAT 462
DB 637 TATCTTAAACCTATGTTGACAGAGAGATTTCATTAACCTGCTGCCAGCTGGGGATTGGAT 696
OY 463 CATATTCGCTGAGAACATTTCTGTCATACCTGATGCCAAATCATATGCTGCTGAACCTT 522
DB 697 CATATTCGCTGAGAACATTTCTGTCATACCTGATGCCAAATCATATGCTGCTGAACCTT 756
OY 523 GTGTGCAAGAAATGTCACCGAGTACCTGTATGATGATGATGATGATGATGATGATGATG 582
DB 757 GTGTGCAAGAAATGTCACCGAGTACCTGTATGATGATGATGATGATGATGATGATGATG 816
OY 583 AGAATGTCAGACAGATTTCTGTGTGAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAG 642
DB 817 AGAATGTCAGACAGATTTCTGTGTGAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAG 876
OY 643 TATTTATTCAAAAC 657
DB 877 TATTTATTCAAAAC 891
XX
XX RESULT 13
XX AAKS1717
XX ID AAKS1717 standard; cDNA; 2366 BP.
XX
XX AAKS1717;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 262.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
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QY	43	TTTTATGATATCCCTCCAGAGAGAAAGACTGATATATGCGAAACCCCTAGGAAATATATA	102
Db	261	TTCCAGAAATTCCTCCAGAGAGAGAAAGCTATATATGCGAAACCCCTAGGAAATATATA	322
QY	103	CCAGAGAGAGATTCACCTTAGACAGACATACAAACAGCTGTGCCAGACTCTGCTTAAACCAA	167
Db	321	CCAGAGAGAGATTCACCTTAGACAGACATACAAACAGCTGTGCCAGACTCTGCTTAAACCAA	380
QY	163	GAAGACGATATGTTTACCAAGCACTGCTATGGAAGACTGAGAAATGTGTGCCCAAAACAAA	222
Db	381	GAAGACGATATGTTTACCAAGCACTGCTATGGAAGACTGAGAAATGTGTGTGCCCAAAACAAA	440
QY	223	CTTGCCAAATGGCACTTCAGATATGATTTGTGCCCAAGCAACGAAACTCTCAGCAAGCTAT	282
Db	441	CTTGCCAAATGGCACTTCAGATATGATTTGTGCCCAAGCAACGAAACTCTCAGCAAGCTAT	500
QY	283	GAAGAGGAAAAAGGAAGCTGTGTGCCAAATATCTTTGAGCAGTGTGTCAGATCAGATCAAGTG	342
Db	501	GAAGAGGAAAAAGGAAGCTGTGTGCCAAATATCTTTGAGCAGTGTGTCAGATCAGATCAAGTG	560
QY	343	GAATTTGTGGACATCTTATATCCCAATATGTGTCCATATGACCAATGGGCACATTAAGTCG	402
Db	561	GAATTTGTGGACATCTTATATCCCAATATGTGTCCATATGACCAATGGGCACATTAAGTCG	620
QY	403	TATCTTAAACCTATGTTGCGAGAGAGATTTCAATACTGCTCTGCCAGCTCGGGGATTGGAT	462
Db	621	TATCTTAAACCTATGTTGCGAGAGAGATTTCAATACTGCTCTGCCAGCTCGGGGATTGGAT	680
QY	463	CATATGCGTCAGAACATTTCTGTGCATACCTGATGCGCAATACATATGCTGTGCTGAACCTT	522
Db	681	CATATGCGTCAGAACATTTCTGTGCATACCTGATGCGCAATACATATGCTGTGCTGAACCTT	740
QY	523	GTGTGCGAAGAGATGTACCGAGCTGACCTCTGATGSCATGCTGTGAGAGAACCTTATCGAG	582
Db	741	GTGTGCGAAGAGATGTACCGAGCTGACCTCTGATGSCATGCTGTGAGAGAACCTTATCGAG	800
QY	583	AGATATGTCAGAGCAGATATCTGTGAGAGAGCGCTGGAGAACGAGAGATGGGGACAG	642
Db	801	AGATATGTCAGAGCAGATATCTGTGTGGAGAGCGCTGTGGAGAACGAGAGATGGGGACAG	860
QY	643	TATTTATTCAAAAAC 657	
Db	861	TATTTATTCAAAAAC 875	
RESULT 15			
AAK52699	AAK52699 standard; cDNA; 3003 BP.		
XX	AAK52699;		
XX	06-NOV-2001 (first entry)		
DE	Human polynucleotide SEQ ID NO 2228.		
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KM	tissue growth factor; immunomodulatory; cancer; leukemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
OS	Homo sapiens.		
PN	MO200157190-A2.		
XX	09-AUG-2001.		
PD			
XX	05-FEB-2001; 2001MO-US04098.		
PF			
XX	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		

PR	15-SEP-2000:	2000US-06633561.
PR	20-OCT-2000:	2000US-0693325.
PR	30-NOV-2000:	2000US-0728422.
XX	(HYSB-) HYSBO INC.	
PA	Tang YT,	Liu C,
PI	Zhao QA,	Meng D,
PI	Xue AJ,	Yang Y,
DR	WPI,	2001-476283/51.
DR	P-PSDB;	AAM73566.
XX	Nucleic acids encoding polypeptides with cytokine-like activities,	
PT	useful in diagnosis and gene therapy -	
XX	Claim 1; Page 4584-4585; 6221pp; English.	
PS	The invention relates to polynucleotides (AAK51456-AAK53435) and the	
CC	encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to	
CC	cytokine, cell proliferation or cell differentiation or which may induce	
CC	production of other cytokines in other cell populations. The	
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or	
CC	peptide therapy. The polypeptides have various cytokine-like activities,	
CC	e.g. stem cell growth factor activity, haematopoiesis regulating	
CC	activity, tissue growth factor activity, immunomodulatory activity and	
CC	activin/inhibn activity and may be useful in the diagnosis and/or	
CC	treatment of cancer, leukemia, nervous system disorders, arthritis and	
CC	inflammation.	
CC	Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK53582) and 3666	
CC	((AAM8020)) are omitted as the relevant pages from the sequence listing	
CC	were missing at the time of publication.	
XX		
SQ	Sequence 3003 BP; 807 A; 703 C; 721 G; 772 T; 0 other;	
Query Match	92.6%; Score 608.6; DB 22; Length 3003;	
Best Local Similarity	99.3%; Pred. No. 1.1e-185;	
Matches 611; Conservative	0; Mismatches 4; Indels 0; Gaps 0	
YY	43 TTTATGAATTCTCAGAGAGAAGACGCTGTATATATAGCGCAACCCTTAGAAGATAA 1020	
DY	11	
DY	298 TTCGAAGATTCTCAGAGAGAAGACGCTGTATATATAGCGCAACCCTTAGAAGATAA 357	
YY	103 CCAGAGAGAAATTCACCTTATGACACATACAACAGCTGTGCCAGACTCTGCTTAACCAA 162	
DY	358 CCAGAGAGAAATTCACCTTATGACACATACAACAGCTGTGCCAGACTCTGCTTAACCAA 417	
YY	163 GAAACAGATGTGTAGCAAGCACTCTTATGAAGACTGGAATTTGTGGCCAACAAA 222	
DY	418 GAAACAGATGTGTAGCAAGCACTCTTATGAAGACTGGAATTTGTGGCCAACAAA 477	
YY	223 CTTGCCAAATGACACTTCACGATGATGTTGTGCCCAAGCAAGGAAATCTCAGCAAGCTAT 282	
DY	478 CTTGCCAAATGACACTTCACGATGATGTTGTGCCCAAGCAAGGAAATCTCAGCAAGCTAT 537	
YY	283 GAAAAAGAAAAGAACTGTGTGCATAAATCTTGGAGAGTGTGAGAGTCAGATCAAGTG 342	
DY	538 GAAAAAGAAAAGAACTGTGTGCATAAATCTTGGAGAGTGTGAGAGTCAGATCAAGTG 597	
YY	343 GAATTTGTGGAACATCTTATATCCCAATGTGTCAATACCAACATGGGCAATAACTCG 402	
DY	598 GAATTTGTGGAACATCTTATATCCCAATGTGTCAATACCAACATGGGCAATAACTCG 657	
YY	403 TATCTTAAACCATATGTGTGACAGAGATTTCAATATGCTGTGCCAGCTGGGGAATGGAT 462	
DY	658 TATCTTAAACCATATGTGTGACAGAGATTTCAATATGCTGTGCCAGCTGGGGAATGGAT 717	
YY	463 CATATCGCTGAACAACTCTGTCAATCACTGGATGCCAAATCACATATGTGCTGGGAATT 522	
DY	718 CATATCGCTGAACAACTCTGTCAATCACTGGATGCCAAATCACATATGTGCTGGGAATT 777	
YY	523 GTGTCCAAAGAAATGATACGAGTACCTCTATATGATGCAATGCTGTGGAAGAAATATCGAG 582	

Db	778	GTGTGCAAGGAATGCTACCGAGTGACCTTGATGGCATGCTGTGGAGAGAACTTATCGAG	837
QY	583	AGAAATGGTCAGAGACAGATTCTGTGTGAGAGGCTGGCAGAAAGAGAGATGGGACAG	642
Db	838	AGAAATGGTCAGAGACAGATTCTGTGTGAGAGGCTGGCAGAAAGAGAGATGGGACAG	897
QY	643	TATTTATTCAAAAAC	657
Db	898	TATTTATTCAAAAAC	912

Search completed: August 20, 2003, 09:41:47
Job time : 200.915 secs

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FEATURES
source

Location/Qualifiers
1. 851
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue="IMAGE:retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by Life
Technologies."

BASE COUNT 243 a 196 c 223 g 188 t 1 others

ORIGIN

Query Match 91.0%; Score 597.6; DB 13; Length 851;
Best Local Similarity 99.2%; Pred. No. 1.3e-157;
Matches 611; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 43 TTTATGAATTCCTCAGAGAGAGAGACTGTATTAATGCGCAACCCCTAGAGATATA 102
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OY 103 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGCAACCCCTAGAGATATA 162
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DB 267 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGCAACCCCTAGAGATATA 326
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OY 163 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGGAATTTGTGGCCAAACAAA 222
327 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGGAATTTGTGGCCAAACAAA 386
OY 223 CTGGCCATGGCAGCTTCAGATATGTTGTGGCCAAAGCGAAACTCTCAGCAAGCTAT 282
|||
DB 387 CTGGCCATGGCAGCTTCAGATATGTTGTGGCCAAAGCGAAACTCTCAGCAAGCTAT 446
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OY 283 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTGAGCAGTGTGAGTGCAGATCAAGT 342
447 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTGAGCAGTGTGAGTGCAGATCAAGT 506
|||
OY 343 GAAATTTGTGAACATCTTATATCCCAATGTGTCAATTAACAACATGGGCACATTAAC 402
507 GAAATTTGTGAACATCTTATATCCCAATGTGTCAATTAACAACATGGGCACATTAAC 566
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|||
DB 567 TATCTTAAACCTATGTGACAGAGATTTCACTGCTGCGCCAGCTCGGGGATTTGAT 626
|||
OY 463 CATATCGCTGAGAACATTTCTGTCACTACCTGGATGCCAATCACTATGTGCTGAACT 522
627 CATATCGCTGAGAACATTTCTGTCACTACCTGGATGCCAATCACTATGTGCTGAACT 686
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OY 523 GTGTGCAAGAGATGTACCGAGTACCTGTGATGGCATGTGTGGAAAGACCTTATGAG 582
687 GTGTGCAAGAGATGTACCGAGTACCTGTGATGGCATGTGTGGAAAGACCTTATGAG 746
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OY 583 AGATGTGCAAGAGATGTACCTGTGAGAGAGCGCTGGCAGAACAGAGATGGGG-ACA 641
747 AGATGTGCAAGAGATGTACCTGTGAGAGAGCGCTGGCAGAACAGAGATGGGGNACA 806
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OY 642 GTATTATTCAAAAAC 657
807 GTATTATTCAAAAAC 822
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DB

RESULT 2
BI822845 828 bp mRNA linear EST 04-OCT-2001
LOCUS 603040168F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180993 5',
DEFINITION mRNA sequence.
ACCESSION BI822845
VERSION BI822845.1 GI:15934395
KEYWORDS EST.

SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC <http://mgl.ncl.nih.gov/>.
TITLE 1 (bases 1 to 828)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM11451 row: h column: 18
High quality sequence stop: 756.

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5180993"
/lab_host="DH10B"
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/note="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age 23-27; 1
male lung, age 27; and 1 male testis, age 66. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

BASE COUNT 241 a 187 c 215 g 185 t

ORIGIN

Query Match 89.0%; Score 585; DB 12; Length 828;
Best Local Similarity 97.9%; Pred. No. 4.5e-154;
Matches 604; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

OY 43 TTTATGAATTCCTCAGAGAGAGAGACTGTATTAATGCGCAACCCCTAGAGATATA 102
|||
DB 188 TTCCAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGCAACCCCTAGAGATATA 247
|||
OY 103 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGCAACCCCTAGAGATATA 162
|||
DB 248 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGCAACCCCTAGAGATATA 307
|||
OY 163 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGGAATTTGTGGCCAAACAAA 222
308 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGGAATTTGTGGCCAAACAAA 367
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OY 223 CTGGCCATGGCAGCTTCAGATATGTTGTGGCCAAAGCGAAACTCTCAGCAAGCTAT 282
368 CTGGCCATGGCAGCTTCAGATATGTTGTGGCCAAAGCGAAACTCTCAGCAAGCTAT 427
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OY 283 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTAGCAGTGTGAGTGCAGATCAAGT 342
428 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTAGCAGTGTGAGTGCAGATCAAGT 487
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DB 488 GAAATTTGTGAACATCTTATATCCCAATGTGTCAATTAACAACATGGGCATTAAC 547
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OY 403 TATCTTAAACCTATGTGACAGAGATTTCACTGCTGCGCCAGCTCGGGGATTTGAT 462
548 TATCTTAAACCTATGTGACAGAGATTTCACTGCTGCGCCAGCTCGGGGATTTGAT 607
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OY 463 CATATCGCTGAGAACATTTCTGTCACTACCTGGATGCCAATCACTATGTGCTGAACT 522
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OY 523 GTGTGCAGGAATGTGTACGAGTACCTCTGTATGCGCATGCTGTGGAGAAGCTTATGAG 582
Db 668 GTGTGCAGGAATGTGTACGAGTACCTCTGTATGCGCATGCTGTGGAGAAGCTTATGAG 727
OY 583 AGAATGTGTGAGACAGATCTGTGTGAGAGGCGCTGGCAGAAAGAGAGA--TGCGGA 639
Db 728 AGAATGTGTGAGACAGATCTGTGTGAGAGGCGCTGGCAGAAAGAGAGACATGGGAGC 787
OY 640 CAGTATTTATTCAAAA 656
Db 788 CAGTATTTATTCAAAA 804

RESULT 3
LOCUS B0948186 1147 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8878641 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6464639
5', mRNA sequence.
ACCESSION B0948186
VERSION B0948186.1 GI:22363664
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1147)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL3986 row: a column: 24
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-Sport6; Site:1; NotI;
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
BASE COUNT 324 a 289 c 284 g 250 t
ORIGIN
Query Match 88.8%; Score 583.2; DB 13; Length 1147;
Best Local Similarity 97.7%; Pred. No. 1.8e-153;
Matches 602; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

OY 223 CTGGCAATGCGACTTCCAGTATGATTTGGCCCAAGCAAGAACTCTCAGCAAGCTAT 282
Db 330 CTGGCAATGCGACTTCCAGTATGATTTGGCCCAAGCAAGAACTCTCAGCAAGCTAT 389
OY 283 GAAAAGAAAAGAACTGTGTCTCAATATCTTTGACAGAGTGTCTCAGATCAATGAG 342
Db 390 GAAAAGAAAAGAACTGTGTCTCAATATCTTTGACAGAGTGTCTCAGATCAATGAG 449
OY 343 GAATTTGTGGAACATCTTATCCCAAGTGTCTTACCAATGCGCAATGAACTG 402
Db 450 GAATTTGTGGAACATCTTATCCCAAGTGTCTTACCAATGCGCAATGAACTG 509
OY 403 TATCTTAAACCTATGTTGAGAGAGATTTCAATACCTGTCTGCCAGCTGGGATTTGAT 462
Db 510 TATCTTAAACCTATGTTGAGAGAGATTTCAATACCTGTCTGCCAGCTGGGATTTGAT 569
OY 463 CATATGCTGTGACACATTTGTGTCTATACCTGTGATGCCAAATACATATGTCTGAACTT 522
Db 570 CATATGCTGTGACACATTTGTGTCTATACCTGTGATGCCAAATACATATGTCTGAACTT 629
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Db 630 GTGTGCAGGAATGTGTACGAGTACCTGTGTATGCGCATGCTGTGGAAGAAGCTTATGCA 689
OY 582 GAGAAATGTGTGAGACAGATTTCTGTGTGAGAGGCGCTGGCAGAAAGAGATGGGAGCA 641
Db 690 GAGAAATGTGTGAGACAGATTTCTGTGTGAGAGGCGCTGGCAGAAAGAGATGGGAGCA 749
OY 642 GATTTATTTCAAAAAC 657
Db 750 GATTTATTTCAAAAAC 765

RESULT 4
LOCUS BG722472 752 bp mRNA linear EST 08-MAY-2001
DEFINITION 602693716F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825970 5',
mRNA sequence.
ACCESSION BG722472
VERSION BG722472.1 GI:14001659
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 752)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (MHRG), Shliraki
Toshnyaki and Piero Carmucci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0739 row: p column: 03
High quality sequence stop: 728.
Location/Qualifiers
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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',

[illegible]

Journal Reference Authors	Year	Page
Journal of Molecular Biology	2002	563-573
Nature	2002	420, 563-573
6 (bases 1 to 2897)		
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Haneqaki, T., Haru, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizumoto, K., Hirooka, T., Hirozane, T., Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kadowa, I., Kasukawa, T., Kato, H., Kawai, J., Kishida, Y., Kondo, S., Kono, H., Kouda, M., Koye, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Onose, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akehira, S., Takeda, Y., Tanaka, T., Tomaru, T., Toy, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
Submitted		
Direct Submission		
Submitted (16-JUL-2001) Yoshitake Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, Fax: 81-45-503-9216)		
COMMENT		
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		
Please visit our web site for further details.		
URL: http://genome.gsc.riken.go.jp/		
URL: http://fantom.gsc.riken.go.jp/		
URL: http://fantom.gsc.riken.go.jp/		
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/sex="male"		
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/clone_id="RIKEN full-length enriched mouse cDNA library		
/dev_stage="adult"		
1. 2897		
/note="beta-transducin repeat containing protein (MGI:1338871, GBNM_009771, evidence: BLASTN, 100%, match=1502)"		
BASE COUNT	720 a	720 g
ORIGIN	736 c	771 g
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Best Local Similarity	90.9%	Pred. No. 6.4e-137;
Matches	559; Conservative	0; Mismatches 56; Indels 0; Gaps 0;
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103	CCAGAGAAATTCCTTAGACAGACATACAAACAGCTGTGCCAGACTGTCTTAACCA	162
279	CCAGAGAAATTCCTTAGACAGACATACAAACAGCTGTGCCAGACTGTCTTAACCA	338
163	GAACAGATTTTATGAGCAAGACAGCTGTCTTAAGACTGTCTGTGCCCAAAACAAA	222
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283	GAAGAGCAAGCAAGCAAGTGTGTCAAAATCTTTGAGCAGGTGTGACATCAAGTGTG	342
459	GAGAGCAAGCAAGCAAGTGTGTCTCAAAATCTTTGAGCAGGTGTGACATCAAGTGTG	518

QY 343 GAATTTGTGGAACATCTTATATCCCAATGTCATTACCAACATGGGCACATTAACCTCG 402
 DB 519 GAAATTTAGAACACCTATATCCCAATGTCATTACCAACATGGGCACATTAACCTCG 578
 QY 403 TATCTTAACCTATGTCAGAGAGATTTCTTAACTGCTGCGACGCTGGGATCGAT 462
 DB 579 TACTTAACCTATGTCAGAGAGATTTCTTAACTGCTGCGACGCTGGGATCGAT 638
 QY 463 CATATCGCTGAGAACATCTTCTGATACCTGATGCCAAATCATCTATGTCGTGAACCT 522
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 QY 523 GTGTGCAAGCAATGTCATACCTGATGCCAAATCATCTATGTCGTGAACCT 582
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 QY 583 AGAATGTCAGACAGATCTCTGTGAGAGAGCTGCGACAGAACAGAGATGGGACAG 642
 DB 759 AGAATGTCAGACAGATCTCTGTGAGAGAGCTGCGACAGAACAGAGATGGGACAG 818
 QY 643 TATTTATTCACAAAAC 657
 DB 819 TACTTATTCACAAAAC 833
 RESULT 7
 AK052317 4502 bp mRNA linear HTC 05-DEC-2002
 LOCUS Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched
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 protein, full insert sequence.
 ACCESSION AK052317
 VERSION AK052317.1 GI:26095121
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 20499374
 REFERENCE
 AUTHORS Kono, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiyagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
 Yonekura, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multiplexed sequencer
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 20530913
 REFERENCE
 AUTHORS Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Flischnmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nakai, I., Pesole, G.,

Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, R., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M. F., Brownstein, J., Bull, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hotmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaeets, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K. F., Suzuki, H.,
 Toyokawa, K., Wang, R. H., Weitz, C., Whitaker, C., Wilmberg, L.,
 Wyszewski, B., Yoshida, K., Hasegawa, Y., Kawai, H., Kohzuki, S.,
 and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 JOURNAL of 60,770 full-length cDNAs
 PUBMED Nature 420, 563-573 (2002)
 REFERENCE
 AUTHORS 6 (bases 1 to 4502)
 ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P.,
 FUKUDA, S., FURUNO, M., HANAGAKI, T., HARA, A., HASHIZUME, W.,
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 YAMAMOTO, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-rsgsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
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 Best Local Similarity 90.9%; Pred. No. 8.3e-117;
 Matches 559; Conservative 0; Mismatches 56; Gaps 0;

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VERSION			
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ORGANISM			Mus musculus (house mouse)
REFERENCE			
AUTHORS			1 Carninci, P. and Hayashizaki, Y.
TITLE			High-efficiency full-length cDNA cloning
JOURNAL			Meth. Enzymol. 303, 19-44 (1999)
MEDLINE			99279253
PUBMED			10349636
REFERENCE			2
AUTHORS			Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE			Ichih, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL			Normalization and subtraction of cap-trapper-selected cDNAs to
MEDLINE			prepare full-length cDNA libraries for rapid discovery of new genes
PUBMED			Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL			20499374
PUBMED			11042159

REFERENCE AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Teshiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, K., Ozawa, M., Ohara, E., Matsubaki, M., Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawaji, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	Riken integrated sequence analysis (RISA) system - 384 format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861 4
TITLE	4 Kawaji, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Harata, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I., Salto, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Salto, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Futschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiya, H., Kuehl, P., Lewis, S., Matsuo, Y., Nakado, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stuhli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barish, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Galaboldi, M., Gustincich, S., Hill, D., Hochmann, M., Hume, D. A., Kamuya, M., Lee, N. H., Lyons, P., Matsumoto, L., Mashima, J., Mazzarelli, J., Nomberts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-Oka, K., Wang, K. H., Weitz, C., Whitlaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlsu, S. and Hayashizaki, Y.
TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851 5
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
REFERENCE AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (Dases 1 to 2970)
JOURNAL REFERENCE AUTHORS	Adachi, J., Aizawa, K., Akiyama, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Harata, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawaji, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Salto, R., Salto, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, K., Tagawa, A., Takahashi, F., Takeku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyo, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE JOURNAL	Direct Submission Submitted (16-Apr-2002) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/. Location/Qualifiers

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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbsrmail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
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 http://image.llnl.gov
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 Library constructed by Life Technologies. Investigator
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 VERSION BF076123.1 GI:10869667
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 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 521)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
 Pereira,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Keeler,J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 11282978
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross-match with the -m1nscore 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACAT
 BACKWARD: GTTTCACAGTACAGAG
 Plate: 85 row: E column: 23
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 Location/Qualifiers

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Db	180	TTCCAGAAATTCCTCTGAGAGAGAAACAGCTGTATATATATGGGAACCCCTTGGAAATATATA	239
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QY	403	TATCTTAAACGATATGTCAGAGATATTCATAAATGCTCTGCCACTGGGGATTTGGAT	462
Db	540	TATCTTAAACGATATGTCAGAGATATTCATAAATGCTCTGCCACTGGGGATTTGGAT	599

Oy	43	TTTATGATTCCTCAGAGAGAAAGACTGTATATATGCGAAACCCCTAGGAAGTATTA	102
Db	238	TTCCAGATTCCTCAGAGAGAAAGACTGTATATATGCGAAACCCCTAGGAAGTATTA	297
Oy	103	CCAGGAAAGATTCACTTAAAGACAGACATCAACAGCTGTGCGAGACTCTGTTAAACCA	162
Db	298	CCAGGAAAGATTCACTTAAAGACAGACTTAAACAGCTGTGCGAGACTCTGTTAAACCA	357

OY	163	GAAACAGATGTTTGGCAGAAGCACTGTGAAGACTGGAATTGTGTGCCAAAACA	222
Dd	358	GAGACAGTATGTCCTACAGACACTGCTTAGAAGCTGAATAATGTGTGCCAAAACA	417
OY	223	CTTGCCATGGCACCTTCCAGTATGATTTGTGCCAACGAAACCTTCAGCAAGCTAT	282
Dd	418	CTTGCCATGGCACCTTCCAGCATGATGTTGTGCCAACGCGGAAACCTTCAGCAAGCTAT	477
OY	283	GAAGAAGAAAAAGAACTGTGTCAAAATCTTTGACAGTGTGCAGACTCAGATCAAGTG	342
Dd	478	GAGAAGGAAAAAGAACTGTGTCAAGTAATTTTGGAGTGTGCAGACTCAGATCAAGTG	537
OY	343	GAAATTTGGACATCTTATATCCCAATGTTGTAATTCGAACAAATGGGCACATAACTCG	402
Dd	538	GAAATTTGAGAACACCTTATATCCCAATGTTGTAATTCGAACAAATGGGCACATCAACTCC	597
OY	403	TATCTTAAACCTATGTTGTCAGAGAGATTTCAACTGCTGTGCCAGCTCGGGGATTTGGAT	462
Dd	598	TACCTAAACCTATGTTGTCAGAGAGATTTCAACTGCTGTGCCAGCTCGGGGATTTGGAC	657
OY	463	CATATCGCTGAGAACATCTGTCTATACCTGATGCCAATACATATGTCGTGAACTT	522
Dd	658	CACATCGCTGAGAACATCTGTCTATACCTGATGCCAATACATGTCGTGAACTT	717
OY	523	GTGTGCAAGAGATGTTACCGAGTACCCTCTGATGGCAGTCTGTGGAAAGACTTAT	578
Dd	718	GTGTGCAAGAGATGTTACCGCTGATCCGCTGACGTGACAGCGGATCTGTGGAAAGACTTAT	773
RESULT 15			
LOCUS	CD350839		
DEFINITION	UT-M-G10-egg-f-10-0-UI.r1 NIH-BMAP_G10 Mus musculus cDNA clone		
IMAGE:	6852971 5', mRNA sequence.		
ACCESSION	CD350839		
VERSION	CD350839.1		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 779) NIH-MGC http://mgc.ncl.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgabbs@remail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mouse1.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: PYX-5. Location/Qualifiers 1..779		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 05:23:39 ; Search time 44.6996 Seconds

(without alignments)
6487.499 Million cell updates/sec

Title: US-10-023-530-1

Percent score: 657
Sequence: 1 atggaccgcggccgagcgct.....gacagatattatcaaac 657

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*
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6: /cgn2_6/ptodata/2/1na/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.4	18.9	126	3	US-09-172-841-2
2	124.4	18.9	126	4	US-08-951-621-2
3	43.8	6.7	7218	1	US-08-232-463-14
4	35.4	5.4	10881	4	US-09-357-206A-9
5	35.4	5.4	12286	4	US-09-357-206A-1
6	34.6	5.3	1848	3	US-08-313-553-10
7	34.6	5.3	1848	3	US-08-767-993-10
8	34.6	5.3	2246	3	US-09-032-742-3
9	34.6	5.3	2246	3	US-09-032-742-21
10	34.6	5.3	2246	3	US-09-032-742-22
11	34.6	5.3	2246	3	US-09-032-742-24
12	34.6	5.3	2246	3	US-09-032-742-25
13	32	4.9	660	4	US-09-134-001C-2805
14	31.6	4.8	4281	4	US-09-357-206A-8
15	30.6	4.7	799	4	US-09-149-476-288
16	30.6	4.7	1002	4	US-09-328-352-3574
17	30.2	4.6	7400	1	US-08-261-663A-1
18	30.2	4.6	7400	5	PCT-US95-0754A-1
19	30	4.6	3540	4	US-09-107-532A-2472
20	29.6	4.5	124884	4	US-09-661-596A-76
21	29.6	4.5	1230025	4	US-09-158-452A-1
22	29.4	4.5	759	4	US-09-328-352-3199
23	29.2	4.4	4693	3	US-09-359-756-1
24	29.2	4.4	7451	1	US-08-684-672-23
25	29.2	4.4	15016	4	US-09-601-198-60
26	29	4.4	552	4	US-09-252-991A-9856
27	29	4.4	821	3	US-08-235-836C-135

28	29	4.4	839	3	US-08-642-807A-30	Sequence 30, Appl
29	29	4.4	3253	4	US-09-759-359A-1	Sequence 1, Appl
30	29	4.4	319608	4	US-09-539-333D-1	Sequence 1, Appl
31	29	4.4	319608	4	US-09-679-409-1	Sequence 1, Appl
32	28.8	4.4	2784	3	US-08-845-256-9	Sequence 9, Appl
33	28.8	4.4	2784	3	US-08-990-571-9	Sequence 9, Appl
34	28.8	4.4	2784	3	US-08-723-142A-9	Sequence 9, Appl
35	28.8	4.4	2784	4	US-09-528-784A-9	Sequence 9, Appl
36	28.6	4.4	2784	4	US-09-569-098A-9	Sequence 9, Appl
37	28.6	4.4	5385	4	US-09-221-017B-972	Sequence 972, App
38	28.4	4.3	1179	3	US-09-247-373B-43	Sequence 43, Appl
39	28.4	4.3	2169	4	US-09-434-408-3	Sequence 27, Appl
40	28.4	4.3	9100	2	US-08-743-637B-27	Sequence 27, Appl
41	28.4	4.3	9100	3	US-08-526-840B-27	Sequence 27, Appl
42	28.4	4.3	1230025	4	US-09-198-452A-1	Sequence 1, Appl
43	28.4	4.3	1830121	4	US-09-557-884-1	Sequence 1, Appl
44	28.4	4.3	1830121	4	US-09-643-980A-1	Sequence 1, Appl
45	28.2	4.3	828	4	US-09-232-160-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-09-172-841-2
; Sequence 2, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-172-841-2

Query Match      18.9%  Score 124.4; DB 3; Length 126;
Beat Local Similarity 99.2%; Pred. No. 2.7e+33;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      442 CTGCCAGCTCGGGGATGGATCATATCGCTGAGAACATTCGTCTACCTGATGCCAA 501
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QY      502 TCACATATGTGCTGCTGAACCTTGTCGAAGAAATGCTACCGATGATCTGATGGCATG 561
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DB      61 TCACATATGTGCTGCTGAACCTTGTCGAAGAAATGCTACCGATGATCTGATGGCATG 120

QY      562 CTGTGG 567
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DB      121 CTGTGG 126

RESULT 2
US-08-951-621-2
; Sequence 2, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
```

```

: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/951,621
: FILING DATE: 16-OCT-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: MacKnight, Kamrin T.
: REGISTRATION NUMBER: 38,230
: REFERENCE/DOCKET NUMBER: BCM-02999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 126 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "DNA"
: US-08-951-621-2

Query Match
Best Local Similarity 18.98; Score 124.4; DB 4; Length 126;
Pred. No. 2,7e-33;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 CTCGACGCTGGGATGTGATCATATGCTGAGAACATCTGTCATACCTGATGCCAA 501
DB 1 CTCGACGCTGGGATGTGATCATATGCTGAGAACATCTGTCATACCTGATGCCAA 60
QY 502 TCACTATGCTGCTGTAACCTGCTGTCGAGAAATGTACGAGTACCTGATGCGATG 561
DB 61 TCACATGCTGCTGTAACCTGCTGTCGAGAAATGTACGAGTACCTGATGCGATG 120
QY 562 CTGTGG 567
DB 121 CTGTGG 126

RESULT 3
US-08-232-463-14/C
: Sequence 14, Application US/08232463
: Patent No. 5670367
: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFLINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 1800 Diagonal Road, Suite 500
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22313-0299
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,463
: FILING DATE:
: CLASSIFICATION: 435
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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/935,313
: FILING DATE:
: APPLICATION NUMBER: EP 91 114 300.6
: FILING DATE: 26-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: BENT, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 30472/114 IMM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-9300
: TELEFAX: (703) 683-4109
: TELEX: 899149
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7218 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CLONE: PT29pl-F15
: US-08-232-463-14

Query Match
Best Local Similarity 6.78; Score 43.8; DB 1; Length 7218;
Pred. No. 0.00022;
Matches 6; Conservative 207; Mismatches 144; Indels 0; Gaps 0;

QY 13 GAGCGGTGCTGCGAGAGGACGACCTCATGTTATGAAATCCGACAGAGAGACTGT 72
DB 1416 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1357
QY 73 AATAATGCGAACCCTAGGAAGATATACAGAGAAATTCATAGACAGACATAC 132
DB 1356 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1297
QY 133 AACAGCTGCCAGACTCTCTTAACCAAGAAAGATATGTTAGCAAGACTGCTATG 192
DB 1296 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1237
QY 193 AAGACGAGAAATGTGTCGCAAAACAACTGCCAATGCACTCCATGATGATGTG 252
DB 1236 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1177
QY 253 CCGAAGCAGAAACTCTCAGCAGAGCTATGAAAGAAAGAAAGACTGTCTCAATAC 312
DB 1176 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1117
QY 313 TTGAGCGAGTGTGAGCTCAGATCATGGAATTTGTGACATCTTATATCCAA 369
DB 1116 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1060

RESULT 4
US-09-357-206A-9/C
: Sequence 9, Application US/09357206A
: Patent No. 6372962
: GENERAL INFORMATION:
: APPLICANT: Dinesh-Kumar, S.
: APPLICANT: Baker, Barbara
: TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Inton Constructs
: FILE REFERENCE: 042250/191805 (5830-5)
: CURRENT FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: US 60/093,494
: PRIOR FILING DATE: 1998-07-20
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 9
: LENGTH: 10881
: TYPE: DNA
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Artificial construct of PN / c-DNA-N / Inton 3 / 3'-GRS
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OTHER INFORMATION: receptor protein (Type 1c).
FEATURE:
  NAME/KEY: misc_signal
  LOCATION: 374
  OTHER INFORMATION: /note="RNA start site."
FEATURE:
  NAME/KEY: CDS
  LOCATION: 376..1734
FEATURE:
  NAME/KEY: terminator
  LOCATION: 1735..1737
  OTHER INFORMATION: /note="serotonin stop codon."
FEATURE:
  NAME/KEY: repeat_region
  LOCATION: 436..462
  OTHER INFORMATION: /note="sequence encoding
  Patent No. 6010885
  OTHER INFORMATION: polypaspartic acid."
FEATURE:
  NAME/KEY: mutation
  LOCATION: replace(1755, "")
  OTHER INFORMATION: /note="C to T mutation removes
  OTHER INFORMATION: AlwNI restriction site."
US-08-767-993-10

Query Match
  Best Local Similarity 5.3%; Score 34.6; DB 3; Length 1848;
  Best Local Similarity 52.4%; Pred. No. 0.15;
  Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 11 CCGAGGCGGTGCTGCAGAGAGACACTTAATTTATGTAATTCCTCAGAGAGAGACT 70
DB 1115 CCGAGAGAGAACTGGCTAATATGAGCCTGACCTTCTGAACTGCTGCAGAGAAAG 1174
OY 71 GTAATAATGCGAAGCCCTAGGAAGATATACAGAGAAGAAATTCACCTTAGACAGACAT 130
DB 1175 GTGGTGAGAGAGAGAAAGCGCTCCGAACCCATTCAGATCAGAAACCACTCGAAGAGA 1234
OY 131 ACAACAGCTGTGCCAGACACTCTGCTT 155
DB 1235 AAGAAAAGCGTCCAGAGGACCAT 1259

RESULT 8
US-09-032-742-3
  Sequence 3, Application US/09032742
  Patent No. 6255089
  GENERAL INFORMATION:
    APPLICANT: Teitler, Milt
    APPLICANT: Herrick-Davis, Katharine
    TITLE OF INVENTION: Constitutively Activated Serotonin
    NUMBER OF SEQUENCES: 25
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Laurence Weinberger
      STREET: 882 S. Malack Street, Suite 103
      CITY: West Chester
      STATE: PA
      COUNTRY: USA
      ZIP: 19380-0053
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/032,742
      FILING DATE: 27-FEB-1998
      CLASSIFICATION: 536
      ATTORNEY/AGENT INFORMATION:
        NAME: Weinberger, Laurence
        REGISTRATION NUMBER: 27,965
```

```
REFERENCE/DOCKET NUMBER: 3086-4
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (610) 431-1703
  TELEFAX: (610) 431-4181
  INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 2246 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
US-09-032-742-3

Query Match
  Best Local Similarity 5.3%; Score 34.6; DB 3; Length 2246;
  Best Local Similarity 52.4%; Pred. No. 0.16;
  Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 11 CCGAGGCGGTGCTGCAGAGAGACACTTAATTTATGTAATTCCTCAGAGAGAGACT 70
DB 1448 CCGAGAGAGAACTGGCTAATATGAGCCTGACCTTCTGAACTGCTGCAGAGAAAG 1507
OY 71 GTAATAATGCGAAGCCCTAGGAAGATATACAGAGAAGAAATTCACCTTAGACAGACAT 130
DB 1508 GTGGTGAGAGAGAGAAAGCGCTCCGAACCCATTCAGATCAGAAACCACTCGAAGAGA 1567
OY 131 ACAACAGCTGTGCCAGACACTCTGCTT 155
DB 1568 AAGAAAAGCGTCCAGAGGACCAT 1592

RESULT 9
US-09-032-742-21
  Sequence 21, Application US/09032742
  Patent No. 6255089
  GENERAL INFORMATION:
    APPLICANT: Teitler, Milt
    APPLICANT: Herrick-Davis, Katharine
    TITLE OF INVENTION: Constitutively Activated Serotonin
    NUMBER OF SEQUENCES: 25
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Laurence Weinberger
      STREET: 882 S. Malack Street, Suite 103
      CITY: West Chester
      STATE: PA
      COUNTRY: USA
      ZIP: 19380-0053
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/032,742
      FILING DATE: 27-FEB-1998
      CLASSIFICATION: 536
      ATTORNEY/AGENT INFORMATION:
        NAME: Weinberger, Laurence
        REGISTRATION NUMBER: 27,965
        REFERENCE/DOCKET NUMBER: 3086-4
        TELECOMMUNICATION INFORMATION:
          TELEPHONE: (610) 431-1703
          TELEFAX: (610) 431-4181
          INFORMATION FOR SEQ ID NO: 21:
            SEQUENCE CHARACTERISTICS:
              LENGTH: 2246 base pairs
              TYPE: nucleic acid
              STRANDEDNESS: single
              TOPOLOGY: linear
            MOLECULE TYPE: DNA (genomic)
US-09-032-742-21
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Query Match 5.3%; Score 34.6; DB 3; Length 2246;
Best Local Similarity 52.4%; Pred. No. 0.16;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 11 CCGAGGGGCTGCTGCAAGAGAGGACCTTATGAAATTCCTCAGAGAGAGACACT 70
DB 1448 CCGAGGAGGAACTGCTATATGAGCCTGAACTTCTGACTGCTGCAAGAGATG 1507
OY 71 GTAATATGCGAAGCCCTAGAGATATACAGAGAAATTCACCTTAGACAGACAT 130
DB 1508 GTGGTAGAGAGAGAGAGAGCTCCGAACCTATATCCAGATCAGAAACACAGCTGGAAGAAGA 1567
OY 131 ACAACAGCTGTGCCAGACTCTGCTT 155
DB 1568 AAGAAAGCGTCCAGAGGACACAT 1592

RESULT 10
US-09-032-742-22
; Sequence 22, Application US/09032742
; Patent No. 6255089
; GENERAL INFORMATION:
; APPLICANT: Teitler, Milt
; APPLICANT: Herrick-Davis, Katharine
; APPLICANT: Egan, Christina C.
; TITLE OF INVENTION: Constitutively Activated Serotonin
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Laurence Weinberger
; STREET: 882 S. Matlack Street, Suite 103
; STREET: P.O. Box 1663
; CITY: West Chester
; STATE: PA
; COUNTRY: USA
; ZIP: 19380-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,742
; FILING DATE: 27-FEB-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinberger, Laurence
; REGISTRATION NUMBER: 27,965
; REFERENCE/DOCKET NUMBER: 3086-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 431-1703
; TELEFAX: (610) 431-4181
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2246 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-032-742-22

Query Match 5.3%; Score 34.6; DB 3; Length 2246;
Best Local Similarity 52.4%; Pred. No. 0.16;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 11 CCGAGGGGCTGCTGCAAGAGAGGACCTTATGAAATTCCTCAGAGAGAGACACT 70
DB 1448 CCGAGGAGGAACTGCTATATGAGCCTGAACTTCTGACTGCTGCAAGAGATG 1507
OY 71 GTAATATGCGAAGCCCTAGAGATATACAGAGAAATTCACCTTAGACAGACAT 130
DB 1508 GTGGTAGAGAGAGAGAGAGCTCCGAACCTATATCCAGATCAGAAACACAGCTGGAAGAAGA 1567

OY 131 ACAACAGCTGTGCCAGACTCTGCTT 155
DB 1568 AAGAAAGCGTCCAGAGGACACAT 1592

RESULT 11
US-09-032-742-24
; Sequence 24, Application US/09032742
; Patent No. 6255089
; GENERAL INFORMATION:
; APPLICANT: Teitler, Milt
; APPLICANT: Herrick-Davis, Katharine
; APPLICANT: Egan, Christina C.
; TITLE OF INVENTION: Constitutively Activated Serotonin
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Laurence Weinberger
; STREET: 882 S. Matlack Street, Suite 103
; STREET: P.O. Box 1663
; CITY: West Chester
; STATE: PA
; COUNTRY: USA
; ZIP: 19380-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,742
; FILING DATE: 27-FEB-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinberger, Laurence
; REGISTRATION NUMBER: 27,965
; REFERENCE/DOCKET NUMBER: 3086-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 431-1703
; TELEFAX: (610) 431-4181
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2246 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-032-742-24

Query Match 5.3%; Score 34.6; DB 3; Length 2246;
Best Local Similarity 52.4%; Pred. No. 0.16;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 11 CCGAGGGGCTGCTGCAAGAGAGGACCTTATGAAATTCCTCAGAGAGAGACACT 70
DB 1448 CCGAGGAGGAACTGCTATATGAGCCTGAACTTCTGACTGCTGCAAGAGATG 1507
OY 71 GTAATATGCGAAGCCCTAGAGATATACAGAGAAATTCACCTTAGACAGACAT 130
DB 1508 GTGGTAGAGAGAGAGAGAGCTCCGAACCTATATCCAGATCAGAAACACAGCTGGAAGAAGA 1567
OY 131 ACAACAGCTGTGCCAGACTCTGCTT 155
DB 1568 AAGAAAGCGTCCAGAGGACACAT 1592

RESULT 12
US-09-032-742-25
; Sequence 25, Application US/09032742
; Patent No. 6255089
; GENERAL INFORMATION:
; APPLICANT: Teitler, Milt

APPLICANT: Herrick-Davis, Katharine
APPLICANT: Egan, Christina C.
TITLE OF INVENTION: Constitutively Activated Serotonin
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Laurence Weinberger
STREET: 882 S. Mallick Street, Suite 103
CITY: West Chester
STATE: PA
COUNTRY: USA
ZIP: 19380-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,742
FILING DATE: 27-FEB-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weinberger, Laurence
REGISTRATION NUMBER: 27,965
REFERENCE/DOCKET NUMBER: 3086-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 431-1703
TELEFAX: (610) 431-4181
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 2246 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-032-742-25

Query Match
Best Local Similarity 5.3%; Score 34.6; DB 3; Length 2246;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

DB 11 CCGAGCGCTGCTGCAGAGAGAGCACTCACTTATGATTCCTCAGAGAGAGACT 70
1448 CCGAGAGAGCACTGCTATATGAGCCCTGAACTTCTGAACTGCTGCAAGAAG 1507

OY 71 GTAATAATGGCGAACCCCTAGAGATAATACAGAGAAATTCATTACAGACAT 130
1508 GTGGTAGAGAGAGAGAGAGCTCCGAACCTTAATCCAGATCAGAAACGCTGAAAGAGA 1567

DB 131 ACAACAGCTGTGCCAGACTCTGCTT 155
1568 AAGAAAGGCTCCAGAGGACCAT 1592

RESULT 13
US-09-134-001C-2805
Sequence 2805, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2805
LENGTH: 660

TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2805

Query Match
Best Local Similarity 4.9%; Score 32; DB 4; Length 660;
Matches 83; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

OY 59 AGAGAGAGAGCTGTATATGCGCAACCCCTAGAGAGATATACAGAGAGATTCAC 118
454 AGATTACATATTATTCAAATGGAACCTTCTTTCAACCAATATCAACAGTCAATCAT 513

DB 119 TTAGACAGACATACACAGCTGTGCCAGACTGCTTAAACCAAGAAACAGATGTTAG 178
514 TTACATACACAGATTAAGAGATACAGATGTTTGCAGTAAAGAAATGAAATTTG 573

OY 179 CAAGCAGCTGTATGAGAGAGTGAATTTGTGGCCAAACAAACTTG 226
574 CAACATGCTTAAAGATACGTGAATATGATGCTCAAAAACAAATTTG 621

RESULT 14
US-09-357-206A-8/C
Sequence 8, Application US/09357206A
Patent No. 6372962
GENERAL INFORMATION:
APPLICANT: Dinesh-Kumar, S.
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REFERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 4281
TYPE: DNA
ORGANISM: Nicotiana glutinosa
US-09-357-206A-8

Query Match
Best Local Similarity 4.8%; Score 31.6; DB 4; Length 4281;
Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

OY 279 CATGAAAAGAAAAGAACTGTGTCAATATTGAGCAGCTGTCAGAGTCAATCA 338
4265 CTCTGAAAAGAAATAGAACTGATGTGAAAAATTTGATTTGTAAGAAAAATATAG 4206

DB 339 ACTGAATTTGTGAACATCTATAT 364
4205 ATGATATTTTCAACAATTTTATAT 4180

RESULT 15
US-09-149-476-288/C
Sequence 288, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER:	60/040,658
EARLER FILING DATE:	1997-03-07
EARLIEST APPLICATION NUMBER:	60/040,334
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040,336
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040,163
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/047,600
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,615
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,597
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,502
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,633
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,583
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,617
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,618
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,503
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,592
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,581
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,584
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,500
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,587
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,492
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,588
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,613
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,582
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,586
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,612
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,632
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,601
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/043,580
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,568
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,671
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,674
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,669
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,312
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,313
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,672

[illegible]

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XX Legrain P, Benarous R, Blot G, Lassot I;
 XX WPI: 2002-508795/54.
 DR P-PSDB; AAU98088.
 XX
 PT Protein-protein complexes for screening drugs or agents that modulate
 PT interaction of proteins, e.g. for identifying the Selected Interacting
 PT Domains (SID), comprises interaction between beta-Trip and Ras Sfl -
 XX
 PS Claim 2; Page 47; 84pp; English.

CC The present invention relates to a new complex of protein-protein
 CC interaction between betatrip (not defined in specification) and Ras Sfl.
 CC The protein-protein complex of the invention is useful for screening
 CC drugs or agents that modulate interaction of proteins. In particular,
 CC the protein complex is useful for identifying the Selected Interacting
 CC Domains (SID). The modulating compounds detected can be used for
 CC treating tumors. The polynucleotides encoding the protein complex may
 CC be used in gene therapy. The present nucleic acid sequence encodes the
 CC human RasSfl protein that was used in the methods of the invention as
 CC a prey protein.
 CC
 XX
 XX

Sequence 1680 BP; 372 A; 433 C; 522 G; 353 T; 0 other:

Query Match 100.0%; Score 1680; DB 24; Length 1680;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCGGGGGGGTGGTGGGGCGGCTACGAGCGGAGAGCTGGGGGAGCGGGGTACGGCTAT 60
 1 CCGGGGGGGTGGTGGGGCGGCTACGAGCGGAGAGCTGGGGGAGCGGGGTACGGCTAT 60
 61 GGGGAGGCGGAGGCGGCTCTTTCGAATGACCTGGAGCAGCAGCAGCAGTGGCTA 120
 61 GGGGAGGCGGAGGCGGCTCTTTCGAATGACCTGGAGCAGCAGCAGCAGTGGCTA 120
 121 CTGAGAGCCAAAGAGACTGCGACTGGAGCTGGAGCAGTCTTCAACCGGGCAACCTGCT 180
 121 CTGAGAGCCAAAGAGACTGCGACTGGAGCTGGAGCAGTCTTCAACCGGGCAACCTGCT 180
 121 CTGAGAGCCAAAGAGACTGCGACTGGAGCTGGAGCAGTCTTCAACCGGGCAACCTGCT 180
 181 AGCTGCGAGCGGCGGCGGAGCAGCAGCAGCTGGAGTGGGAGGAGCAGCTGACCTTTC 240
 181 AGCTGCGAGCGGCGGCGGAGCAGCAGCAGCTGGAGTGGGAGGAGCAGCTGACCTTTC 240
 181 AGCTGCGAGCGGCGGCGGAGCAGCAGCAGCTGGAGTGGGAGGAGCAGCTGACCTTTC 240
 241 TCAAGCTGAGATTGAGCAGAGAGATCAAGAGTACATGCCAGATCAACAGCAACCTTTC 300
 241 TCAAGCTGAGATTGAGCAGAGAGATCAAGAGTACATGCCAGATCAACAGCAACCTTTC 300
 301 CATAGCTTGAACAAGAGCGTCTTACACAGGCTTCAACAGGTTCAAGCTGAAAGCTGCT 360
 301 CATAGCTTGAACAAGAGCGTCTTACACAGGCTTCAACAGGTTCAAGCTGAAAGCTGCT 360
 301 CATAGCTTGAACAAGAGCGTCTTACACAGGCTTCAACAGGTTCAAGCTGAAAGCTGCT 360
 361 GCGGCGCTGCTCTGCGCCCTCCAGCAAGAACCCACCTCTTGAGAGATGCGGGCGGG 420
 361 GCGGCGCTGCTCTGCGCCCTCCAGCAAGAACCCACCTCTTGAGAGATGCGGGCGGG 420
 361 GCGGCGCTGCTCTGCGCCCTCCAGCAAGAACCCACCTCTTGAGAGATGCGGGCGGG 420
 421 CCCAGAGAGGGGCGCAAGTGTCAAGCGCGGCACTTCTTAACTGGCCCAAGATGCTGT 480
 421 CCCAGAGAGGGGCGCAAGTGTCAAGCGCGGCACTTCTTAACTGGCCCAAGATGCTGT 480
 421 CCCAGAGAGGGGCGCAAGTGTCAAGCGCGGCACTTCTTAACTGGCCCAAGATGCTGT 480
 481 CAAGCAGCTGATGCTGCTGACGACACAGGGCAGCTGAAGTCAATTGAGCGGCTGCTCG 540
 481 CAAGCAGCTGATGCTGCTGACGACACAGGGCAGCTGAAGTCAATTGAGCGGCTGCTCG 540
 481 CAAGCAGCTGATGCTGCTGACGACACAGGGCAGCTGAAGTCAATTGAGCGGCTGCTCG 540
 541 AAAGTTCTGTTGGTGGATGACCCCGCAAGTTGCACTCTTAAAGGCGCGTGAGCTGCA 600
 541 AAAGTTCTGTTGGTGGATGACCCCGCAAGTTGCACTCTTAAAGGCGCGTGAGCTGCA 600
 541 AAAGTTCTGTTGGTGGATGACCCCGCAAGTTGCACTCTTAAAGGCGCGTGAGCTGCA 600
 601 CGGCCAAGTGTACTTGGGGAAGCTGTTGATGATGAGAGCCCTGCGGCTGCGGCTCT 660
 601 CGGCCAAGTGTACTTGGGGAAGCTGTTGATGATGAGAGCCCTGCGGCTGCGGCTCT 660

661 GGCAGGGCCAGTAGACAAGGCCCTGAGCTTTGCTCTGAAGAAAATGACTCTGGGAGCT 720
 661 GGCAGGGCCAGTAGACAAGGCCCTGAGCTTTGCTCTGAAGAAAATGACTCTGGGAGCT 720
 721 GAACTGGAGCCCTTACAGATGCTGAACTGAACTGAACTGCTTCTAGTATCTCTGACGGGA 780
 721 GAACTGGAGCCCTTACAGATGCTGAACTGAACTGAACTGCTTCTAGTATCTCTGACGGGA 780
 721 GAACTGGAGCCCTTACAGATGCTGAACTGAACTGAACTGCTTCTAGTATCTCTGACGGGA 780
 781 GGAGGAGAGGACCTCCGCGAGATCTGCAAGATGCTGCTTATGCGCGCAGGAATGCA 840
 781 GGAGGAGAGGACCTCCGCGAGATCTGCAAGATGCTGCTTATGCGCGCAGGAATGCA 840
 781 GGAGGAGAGGACCTCCGCGAGATCTGCAAGATGCTGCTTATGCGCGCAGGAATGCA 840
 841 AGAGCCCTGACAGCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 841 AGAGCCCTGACAGCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 841 AGAGCCCTGACAGCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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 961 GAGTGTGATGAGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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 961 GAGTGTGATGAGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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 1021 TGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 1081 TACTGGGCGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1140
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 1081 TACTGGGCGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1140
 1141 GGTGAGAGAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 1141 GGTGAGAGAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 1141 GGTGAGAGAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 1201 AACAGAACAGGCTGATGTTTCCAGGGGTGACGGGCTGCTATGAGAGAAAGTTTGA 1260
 1201 AACAGAACAGGCTGATGTTTCCAGGGGTGACGGGCTGCTATGAGAGAAAGTTTGA 1260
 1201 AACAGAACAGGCTGATGTTTCCAGGGGTGACGGGCTGCTATGAGAGAAAGTTTGA 1260
 1261 TCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 1261 TCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 1261 TCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 1321 AGGCTATGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 1321 AGGCTATGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 1321 AGGCTATGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 1381 TCAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 1381 TCAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 1381 TCAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 1441 CCTGGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 1441 CCTGGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 1441 CCTGGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 1501 CAAAGCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 1501 CAAAGCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 1501 CAAAGCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 1561 GGTGGCTGAGCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 1561 GGTGGCTGAGCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
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 1621 CCTGGGCGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680

RESULT 2
 ABS5576
 ID ABS5576 standard; cDNA; 1692 BP.
 XX

AC ABSS5576;
XX 19-DEC-2002 (first entry)
XX Human cDNA encoding tumour suppressor RASSFL1.C.
DE
XX
XX Human; ss; gene; tumour suppressor; RASSFL1.C; cancer; breast cancer;
KM DNA methylation; lung cancer; kidney cancer; ovarian cancer;
XX head and neck cancer; melanoma; chromosome 3p21.3.
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 12..824
XX /tag="a
XX /product="RASSFL1.C"
XX
XX US2002098530-A1.
XX
XX 25-JUL-2002.
XX
XX 30-MAR-2001; 2001US-0821803.
XX
XX 30-MAR-2000; 2000US-193268P.
XX
XX (CITY) CITY OF HOPE.
XX
XX Pfeiffer GP, Dammann R;
XX
XX WPI: 2002-690479/74.
XX P-PSDB: ABG71309.
XX
XX Novel tumor suppressor gene, termed RASSFL1, useful for the diagnosis of
XX predisposition to cancer by analyzing its methylation status,
XX heterozygosity or mutation
XX
XX
XX Claim 2: Page 32-34; 57pp; English.
XX
XX The invention relates to an isolated tumour suppressor gene coding for
XX splice variant RASSFL1.A, RASSFL1.B or RASSFL1.C protein or its complement,
XX or a DNA molecule which hybridises under stringent conditions to them.
XX Also included are naturally occurring mutants of RASSFL1.A, detecting (M1)
XX a methylated RASSFL1 gene, non-expressed RASSFL1 gene or an alteration in
XX RASSFL1 where the methylation, non-expression or alteration is associated
XX with cancer in a human, by analysing an RASSFL1 gene or an RASSFL1 gene
XX expression product from a tissue or body fluid of the human;
XX administering RASSFL1 agonists to treat cancer, a RASSFL1 non-human
XX transgenic animal, a cell line from the transgenic animal, and
XX screening for cancer therapeutics/drug candidates useful in treating
XX cancer resulting from a methylated or a mutation in RASSFL1.
XX (M1) is useful for detecting methylated RASSFL1 gene, which is
XX useful for determining whether a human subject has or is at risk for
XX developing cancer. The method involves detecting the methylation or
XX non-expression of the gene or the presence or absence of a genetic
XX polymorphism as in the RASSFL1 gene of the subject, where the
XX methylation or non-expression or the presence of the genetic
XX polymorphism identifies a subject that has or is at risk for developing
XX cancer. The mutants are useful for screening for drug candidates useful
XX in treating cancer resulting from the RASSFL1 gene. Analysis of the RASSFL1
XX gene is useful in the diagnosis of predisposition to cancer, including
XX lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
XX association between the RASSFL1 gene and cancer permits the early
XX pre-symptomatic screening of individuals to identify those at risk for
XX developing cancer. RASSFL1 protein is useful for identifying agonists of
XX the biological function of an RASSFL1 protein. RASSFL1, its encoding
XX nucleic acids, antibodies and compounds identified by the screening
XX assays are useful for treating cancer. The gene for RASSFL1 is located
XX on chromosome 3p21.3. The present sequence encodes the RASSFL1 splice
XX variant RASSFL1.C.
XX
XX Sequence 1692 BP; 424 A; 423 C; 498 G; 347 T; 0 other;
XX
XX Query Match 95.4%; Score 1602.6; DB 24; Length 1692;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 4; Indels 3; Gaps 2;
QY 48 CGGGTAGGGCTATGGGCGAGGGAGGCGCCCTTCTTGAATAAGACTGGAGCAGACGA 107
DB 1 CGGGTAGGGCTATGGGCGAGGGAGGCGCCCTTCTTGAATAAGACTGGAGCAGACGA 60
QY 108 CGAGAGTGGCTACTGACAGCCAAAGAGTCCGAGCTCGAGAGTCCAGAGTACTTCCAG 167
DB 61 CGAGAGTGGCTACTGACAGCCAAAGAGTCCGAGCTCGAGAGTCCAGAGTACTTCCAG 120
QY 168 CGGAACTTCCTGCTAGCTCCAGGCGCGCGCGGAGCAGAGAGCTTGGAGTGGAGA 227
DB 121 CGGAACTTCCTGCTAGCTCCAGGCGCGCGCGGAGCAGAGAGCTTGGAGTGGAGA 180
QY 228 CAGCTGACCTTCTCAAGGTGAGATGAGCAGAGAAATCAAGGATGCAATGGCCCAATCA 287
DB 181 CAGCTGACCTTCTCAAGGTGAGATGAGCAGAGAAATCAAGGATGCAATGGCCCAATCA 240
QY 288 ACAGCAACCTTTCATGATGATGAAACAGAGAGCTTCTTACAGAGCTTCAATCAAGTTC 347
DB 241 ACAGCAACCTTTCATGATGATGAAACAGAGAGCTTCTTACAGAGCTTCAATCAAGTTC 300
QY 348 AGCTGAAGTGGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407
DB 301 AGCTGAAGTGGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 408 ATGGCCGG 467
DB 361 ATGGCCGG 420
QY 468 CCAAGAGTCTGTCAAGCACTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
DB 421 CCAAGAGTCTGTGTCAAGCACTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 528 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 587
DB 481 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 588 GGGCTGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 647
DB 541 GGGCTGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 600
QY 648 GGGCTGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 707
DB 601 GGGCTGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 660
QY 708 ACTCTGGGAGGTGAAGTGGAGGCTTCAAGTGGCTGCAAGTGGCTGCAAGTGGCTG 767
DB 661 ACTCTGGGAGGTGAAGTGGAGGCTTCAAGTGGCTGCAAGTGGCTGCAAGTGGCTG 720
QY 768 TCGTGGAGGG 827
DB 721 TCGTGGAGGG 780
QY 828 GCCAGAGATCCAGAGGCGCTGACGCTGCGCCCTTGGGAGCTCTTGAACCCAG 887
DB 781 GCCAGAGATCCAGAGGCGCTGACGCTGCGCCCTTGGGAGCTCTTGAACCCAG 840
QY 888 GTGGAGGAGACAGACGAGGAGCGCCCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 947
DB 841 GTGGAGGAGACAGACGAGGAGCGCCCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 948 GGGCGTGGAGTGAATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1007
DB 901 GGGCGTGGAGTGAATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 960
QY 1008 CAGCGAAGTGAATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1067
DB 961 CAGCGAAGTGAATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1020
QY 1068 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1127


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OY 490 GCATGCTGTCACGACAGGCGACGTGAAGTCATGTAGGCCCTGCTCGAAAGTCTT 549
    |||
DB 680 ACATGTGCTGTCACGACAGGCGACGTGAAGTCATGTAGGCCCTGCTCGAAAGTCTT 739
OY 550 GGTGGGATGACCCCGCAAGTTTGCACTTTTGAGCGCGCTGAGCGCTCAGCGCCAACT 609
    |||
DB 740 GGTGGGATGACCCCGCAAGTTTGCACTTTTGAGCGCGCTGAGCGCTCAGCGCCAACT 799
OY 610 GTACTTTCGGAAGCTGTTGGATGATGAGCAGCCCGCTGCGGCTCTGCGCAGAGGCC 669
    |||
DB 800 GTACTTTCGGAAGCTGTTGGATGATGAGCAGCCCGCTGCGGCTCTGCGCAGAGGCC 859
OY 670 CAGTGACAAAGCCCTGAGCTTGTCTCTGAGGAAAATGACTTGGGAGGTGAATGGGA 729
    |||
DB 860 CAGTGACAAAGCCCTGAGCTTGTCTCTGAGGAAAATGACTTGGGAGGTGAATGGGA 919
OY 730 GCGCTTCAGACGCTGGAACCTACATTAATCTTACTATACCTGACGCGGAGAGAGAGA 789
    |||
DB 920 GCGCTTCAGACGCTGGAACCTACATTAATCTTACTATACCTGACGCGGAGAGAGAGA 979
OY 790 GCACCTCCGCGACATCTGACAAAGTACTCTATTGCGCGCAGAAAGATCCAGAGGCCCT 849
    |||
DB 980 GCACCTCCGCGACATCTGACAAAGTACTCTATTGCGCGCAGAAAGATCCAGAGGCCCT 1039
OY 850 GCACGCGCTGCGCCCTTGGGTGACCTTGTACCCCGAGGTGGAAGGACAGACAGCAGCAG 909
    |||
DB 1040 GCACGCGCTGCGCCCTTGGGTGACCTTGTGTACCCCGAGGTGGAAGGACAGACAGCAGCAG 1099
OY 910 CCGCAGATGCGTCCGCTGTGATGTGACAGGCGCACTGGGCGCTGTGGAATGAGTGTGA 969
    |||
DB 1100 CCGCAGATGCGTCCGCTGTGATGTGACAGGCGCACTGGGCGCTGTGGAATGAGTGTGA 1159
OY 970 TGGAGGCGCTGCTGCTGGGGGAATGAGCCCAAGACAGCAGCAAGTACTGCTCCCTG 1029
    |||
DB 1160 TGGAGGCGCTGCTGCTGGGGGAATGAGCCCAAGACAGCAGCAAGTACTGCTCCCTG 1219
OY 1030 TGTCCACTATGAGGTGTGACCAAGTATGGCTCTGCAACCCCTGCTCATTAATGAGGCC 1089
    |||
DB 1220 TGTCCACTATGAGGTGTGACCAAGTATGGCTCTGCAACCCCTGCTCATTAATGAGGCC 1279
OY 1090 TTAGTGGGCGAGGCGCCCTGAGAAAGTGTCCAGAGCGCTGACAGCAGAGAGTGTGAGAC 1149
    |||
DB 1280 TTAGTGGGCGAGGCGCCCTGAGAAAGTGTCCAGAGCGCTGACAGCAGAGAGTGTGAGAC 1339
OY 1150 AGAAGTCTCTCAATTTTGTCTCAGAAAGTGAATAATCTTGGAGACCCCTCAACAGACAGA 1209
    |||
DB 1340 AGAAGTCTCTCAATTTTGTCTCAGAAAGTGAATAATCTTGGAGACCCCTCAACAGACAGA 1399
OY 1210 GGGTCATGTTTGCAGGCGGTGACGCGCCCTCATCTATGAGGAAAAGTTTGGATCTGAATG 1269
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DB 1400 GGGTCATGTTTGCAGGCGGTGACGCGCCCTCATCTATGAGGAAAAGTTTGGATCTGAATG 1459
OY 1270 TGGTCTCAGGATATCTTATCAGAGTAAAGGGGTGCTCGAATAAAGCAGGACTTGA 1329
    |||
DB 1460 TGGTCTCAGGATATCTTATCAGAGTAAAGGGGTGCTCGAATAAAGCAGGACTTGA 1519
OY 1330 GGAAGAGCTGTTGTTCTCTACAGTGCACACTCTCAACACACCTCTGAGGTGAGGAGT 1389
    |||
DB 1520 GGAAGAGCTGTTGTTCTCTACAGTGCACACTCTCAACACACCTCTGAGGTGAGGAGT 1579
OY 1390 GGTGCTCAGATGACAGATGTGCTTAAATGCTTCAATATGAGAGAGATGCTCCCTGGGCCA 1449
    |||
DB 1580 GGTGCTCAGATGACAGATGTGCTTAAATGCTTCAATATGAGAGAGATGCTCCCTGGGCCA 1639
OY 1450 GGGTCTGTGTGATGATGGGCGACGCGCCAGGTTCATACCTTATTTCTATCAAAAGCAG 1509
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DB 1640 GGGTCTGTGTGATGATGGGCGACGCGCCAGGTTCATACCTTATTTCTATCAAAAGCAG 1699
OY 1510 GGTCTCTCCCTCAGGTGTTTATGAAAGTGCATGATGATGATGATGATGATGATGATGATG 1569
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DB 1700 GGTCTCTCCCTCAGGTGTTTATGAAAGTGCATGATGATGATGATGATGATGATGATGATG 1759

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OY 1570 ACCTGAATCCCTCTCTGCGGAAAGGGGTTGGGGTGACAGTCATCATCAGG--CTTGGGG 1627
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OY 1628 CTGAGAGAAATGGCTCAATTAAGATTTCAAGATTCACAAAATTAATTAATTAATTAATTA 1680
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DB 1820 CTGAGAGAAATGGCTCAATTAAGATTTCAAGATTCACAAAATTAATTAATTAATTAATTA 1872

RESULT 4
ABS55591
ID ABS55591 standard; cDNA: 1873 BP.
XX
AC ABS55591;
XX
DT 19-DEC-2002 (first entry)
XX
DE Human cDNA encoding tumour suppressor RASFP1.A variant 1.
XX
KW Human; ss; gene; tumour suppressor; RASFP1.A; cancer; breast cancer;
KW SNP; single nucleotide polymorphism; DNA methylation; lung cancer;
KW kidney cancer; ovarian cancer; head and neck cancer; melanoma;
KW chromosome 3p21.3.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 39..1061
FT /tag= a
FT /product= "RASFP1.A"
FT /replac= (99,C)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT variation /tag= c
FT
FT
PN US2002098530-A1.
XX
PD 25-JUL-2002.
XX
PF 30-MAR-2001; 2001US-0821803.
XX
PR 30-MAR-2000; 2000US-193268P.
XX
PA (CITY ) CITY OF HOPE.
XX
PI Pfeiffer GP, Dammann R;
XX
DR WPI; 2002-690479/74.
XX
DR P-PSDB; ABG71310.
XX
PT Novel tumor suppressor gene, termed RASFP1, useful for the diagnosis of
PT predisposition to cancer by analyzing its methylation status,
PT heterozygosity or mutation -
XX
PS Claim 3; Page -: 57pp; English.
XX
XX
The invention relates to an isolated tumour suppressor gene coding for
CC splice variant RASFP1.A, RASFP1.B or RASFP1.C protein or its complement,
CC or a DNA molecule which hybridises under stringent conditions to them.
CC Also included are naturally occurring mutants of RASFP1.A, detecting (M1)
CC a methylated RASFP1 gene, non-expressed RASFP1 gene or an alteration in
CC RASFP1 where the methylation, non-expression or alteration is associated
CC with cancer in a human, by analysing an RASFP1 gene or an RASFP gene
CC expression product from a tissue or body fluid of the human;
CC administering RASFP1 agonists to treat cancer, a RASFP1 non-human
CC transgenic animal, a cell line from the transgenic animal, and
CC screening for cancer therapeutics/drug candidates useful in treating
CC cancer resulting from a methylated or a mutation in RASFP1.
CC (M1) is useful for detecting methylated RASFP1 gene, which is
CC useful for determining whether a human subject has or is at risk for
CC developing cancer. The method involves detecting the methylation or
CC non-expression of the gene or the presence or absence of a genetic

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FT      /product= "RASSF1.A"
FT      replace (99,C)
FT      /tag= b
FT      /standard_name= "Single nucleotide polymorphism"
FT      /replace (442,'T')
FT      variation
FT      /tag= c
XX      US2002098530-A1.
XX      .
XX      25-JUL-2002.
XX      30-MAR-2001; 2001US-0821803.
XX      30-MAR-2000; 2000US-193268P.
XX      (CITY ) CITY OF HOPE.
XX      Pfelfer GP, Dannmann R;
XX      MPI; 2002-690479/74.
XX      P-PSDB; ABG71311.
XX      Novel tumor suppressor gene, termed RASSF1, useful for the diagnosis of
XX      predisposition to cancer by analyzing its methylation status,
XX      heterozygosity or mutation
XX      .
XX      Claim 3; Page -: 57pp; English.
XX      .
XX      The invention relates to an isolated tumour suppressor gene coding for
XX      splice variant RASSF1.A, RASSF1.B or RASSF1.C protein or its complement,
XX      or a DNA molecule which hybridises under stringent conditions to them.
XX      Also included are naturally occurring mutants of RASSF1.A, detecting (M1)
XX      a methylated RASSF1 gene, non-expressed RASSF1 gene or an alteration in
XX      RASSF1 where the methylation, non-expression or alteration is associated
XX      with cancer in a human, by analysing an RASSF1 gene or an RASSF gene
XX      expression product from a tissue or body fluid of the human;
XX      administering RASSF1 agonists to treat cancer, a RASSF1 non-human
XX      transgenic animal, a cell line from the transgenic animal, and
XX      screening for cancer therapeutics/drug candidates useful in treating
XX      cancer resulting from a methylated or a mutation in RASSF1.
XX      (M1) is useful for detected methylated RASSF1 gene, which is
XX      useful for determining whether a human subject has or is at risk for
XX      developing cancer. The method involves detecting the methylation or
XX      non-expression of the gene or the presence or absence of a genetic
XX      polymorphism as in the RASSF1 gene of the subject, where the
XX      methylation or non-expression or the presence of a genetic
XX      polymorphism identifies a subject that has or is at risk for developing
XX      cancer. The mutants are useful for screening for drug candidates useful
XX      in treating cancer resulting from the RASSF1 gene. Analysis of the RASSF1
XX      gene is useful in the diagnosis of predisposition to cancer, including
XX      lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
XX      association between the RASSF1 gene and cancer permits the early
XX      presymptomatic screening of individuals to identify those at risk for
XX      developing cancer. RASSF1 protein is useful for identifying agonists of
XX      the biological function of an RASSF1 protein. RASSF1, its encoding
XX      nucleic acids, antipodides and compounds identified by the screening
XX      assays are useful for treating cancer. The gene for RASSF1 is located
XX      on chromosome 3p21.3. The present sequence encodes a natural variant of
XX      RASSF1 splice variant RASSF1.A.
XX      Note: The present sequence is not shown in the specification but
XX      was created by the indexer using the information in claim 3 and the
XX      RASSF1.A sequence appearing as AB555574.
XX      .
XX      Sequence 1873 BP; 394 A; 517 C; 585 G; 377 T; 0 other;
XX      .
XX      Query Match      86.6%; Score 1455; DB 24; Length 1873;
XX      Best Local Similarity 98.9%; Pred. NO. 0;
XX      Matches 1476; Conservative 0; Mismatches 15; Indels 2; Gaps 1
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XX      190 GCCGGCGCCGGACACGAGACCTGTGTGAGTGGAGACACCTGACCTTTCTCAAGCTGA 249
XX      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY	250	GATTGAGCAGAAAGATCAAGAGGTACATATGCCAGATCAACAGCAACTCTTCATAGACTT	309
Db	440	GACTGAGCAGAAAGATCAAGAGGTACAAATGCCAGATCAACAGCAACTCTTCATAGACTT	499
QY	310	GAACAGAGCAGGTTCCTACAGAGCTTCATCAAGGTATGAGCTGAAAGCGTGGGCGCCGT	369
Db	500	GAACAGAGCAGGTTCCTACAGAGCTTCATCAAGGTATGAGCTGAAAGCGTGGGCGCCGT	559
QY	370	CTCTGTGCCCTCCACAGCAAGGCCACCCCTCCCTGAGAGATGCCGGCGGGGCCAGAGC	429
Db	560	CTCTGTGCCCTCCACAGCAAGGCCACCCCTCCCTGAGAGATGCCGGCGGGGCCAGAGC	619
QY	430	GGGCACAAGTGTCAAGCGCCCGCACTTCTTTTACCTGCCCAAGAGTCTGTCAAGCACCT	489
Db	490	GCATGTGTGTTCAGCCACAAAGGGCAGTGAAGTCAATTGAGGCCCGCGCGCCAAAGTTCTT	549
QY	550	GGTGTGTGATGACCCCGCCCAAGTTTGCACCTCTTTTACGCGCCCTGAGCTCAAGGCCAAGT	609
Db	740	GSTGTATATGACCCCCCGCAGTTTGCACCTCTTTAGGCGCCTGAGCCTCAAGGCCAAGT	799
QY	610	GTACTTGGCGAAGCTGTTGATGATGAGCAGGCCCTGCGGCTGCGGCTCTGCGAGGGCC	669
Db	800	GTACTTGGCGAAGCTGTTGATGATGAGCAGGCCCTGCGGCTGCGGCTCTGCGAGGGCC	859
QY	670	CAGTGACAAAGCCCTGAGCTTTGTCTCTAAGAAATATACATCTGGGGAGGTGMACTGGGA	729
Db	860	CAGTGACAAAGCCCTGAGCTTTGTCTCTAAGAAATATACATCTGGGGAGGTGMACTGGGA	919
QY	730	CGCCTTCAGCATGCCCTGAACACTACATAATCTCTACGTATCTGTGACGCGGAGSAGAGAGA	789
Db	920	CGCCTTCAGCATGCCCTGAACACTACATAATCTCTACGTATCTGTGACGCGGAGSAGAGAGA	979
QY	790	GCACCTCCGCCAGATCTGCGAGAGTACTCTTATTCGCCCGCAAGAAAGATCCAAAGGCCCT	849
Db	980	GCACCTCCGCCAGATCTGCGAGAGTACTCTTATTCGCCCGCAAGAAAGATCCAAAGGCCCT	1039
QY	850	GCAGCCCGCCCCCTTTGGGTACCTCTTGTACCCCCAGGTGGAAAGGCACAGCAGGCGAG	909
Db	1040	GCAGCCCGCCCCCTTTGGGTACCTCTTGTACCCCCAGGTGGAAAGGCACAGCAGGCGAG	1099
QY	910	CGCCCAAGTGCCTGCGGTGAGTGTGACAGGGCCAGTGGGGCCTTGGAAATGAGTGTCA	969
Db	1100	CGCCCAAGTGCCTGCGGTGAGTGTGACAGGGCCAGTGGGGCCTTGGAAATGAGTGTCA	1159
QY	970	TGAGAGCCCTCTGTGTGTGGGGGAATGAGCCAGAAACAGCGAAGTACTGTCCTCTG	1029
Db	1160	TGAGAGCCCTCTGTGTGTGGGGGAATGAGCCAGAAACAGCGAAGTACTGTCCTCTG	1219
QY	1030	TGTCACCTATGGGTGTAGCCAGGTATGGCTGTGACCCCTCTGCGCTCATTTACTGGGCC	1089
Db	1220	TGTCACCTATGGGTGTAGCCAGGTATGGCTGTGACCCCTCTGCGCTCATTTACTGGGCC	1279
QY	1090	TTAGTGGGCCAGGGCTGCGCTGAGAAAGTGTCCAGGGCTGAGAGAGAGTGGTTCACAG	1149
Db	1280	TTAGTGGGCCAGGGCTGCGCTGAGAAAGTGTCCAGGGCTGAGAGAGAGTGGTTCACAG	1339
QY	1150	AGAACTCTCTCAATTTTTGTCTCGAAAGTGAATACTTGGAGCCCTGCAACAGAAC	1209
Db	1340	AGAACTCTCTCAATTTTTGTCTCGAAAGTGAATACTTGGAGCCCTGCAACAGAAC	1399
QY	1210	GGGTATATTTTGCAGGGGTGAGCGCCCTCATCTATAGAGAAAGTTTGGATCTTGAATG	1269
Db	1400	GGGTATATTTTGCAGGGGTGAGCGCCCTCATCTATAGAGAAAGTTTGGATCTTGAATG	1459
QY	1270	TGGTTCAGAGATATCTTATCAGAGCTAAAGGTGGGTGCTCAGAAATAGGACAGCATTTGA	1329
Db	1460	TGGTTCAGAGATATCTTATCAGAGCTAAAGGTGGGTGCTCAGAAATAGGACAGCATTTGA	1519
QY	1330	GGAAAGTCTTGGTTCTCTCTACAGTCCAACTCTCACAACACCCTGAGTCAAGGAGT	1389

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DB 1520 GGAAGAGTCTGGTCTCTCTACAGTCCAACTCTACACACCTTAGGTCAGGAGT 1579
OY 1390 GCTGCTCAGACAGTACAGCATGTCCTTAATGCTTATGAGAGAGATGTCCTGGGCA 1449
DB 1580 GCTGCTCAGACAGTACAGCATGTCCTTAATGCTTATGAGAGAGATGTCCTGGGCA 1639
OY 1450 GGGTGTGTGTAATGTGGGACATGCCCCAGATTCATTTGCTTAATCAAGCCAG 1509
DB 1640 GGGTGTGTGTAATGTGGGACATGCCCCAGATTCATTTGCTTAATCAAGCCAG 1699
OY 1510 GGTCTCTCCCTCAGGTGTTTTTATGAAGTGGTGAATGTATGTAATGTGGTGGCTC 1569
DB 1700 GGTCTCTCCCTCAGGTGTTTTTATGAAGTGGTGAATGTATGTAATGTGGTGGCTC 1759
OY 1570 AGCTGAATGCTCTCTGTGGGGAAGGGGTTGGGTTGACAGTCAATCAGCAG--CCTGGAG 1627
DB 1760 AGCTGAATGCTCTCTGTGGGGAAGGGGTTGGGTTGACAGTCAATCAGCAGCCTGGAGC 1819
OY 1628 CTGAGAGAAATGGCTCAATTAAGATTCATCAAGTCCAAAAAAGAAAAA 1680
DB 1820 CTGAGAGAAATGGCTCAATTAAGATTCATCAAGTCCAAAAAAGAAAAA 1872

RESULT 6
ABSS5593
ID ABSS5593 standard; CDNA; 1873 BP.
XX
AC ABSS5593;
XX
DT 19-DEC-2002 (first entry)
XX
DE Human CDNA encoding tumour suppressor RASSFL.A variant 3.
XX
KW Human; ss; gene; tumour suppressor; RASSFL.A; cancer; breast cancer;
KW SNP; single nucleotide polymorphism; DNA methylation; lung cancer;
KW kidney cancer; ovarian cancer; head and neck cancer; melanoma;
KW chromosome 3p21.3.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 39..1061
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FT /product= "RASSFL.A"
FT /tag= b
FT /replace (99,C)
FT /standard_name= "Single nucleotide polymorphism"
FT /replace (808,G)
FT /tag= c
XX
PN US2002098530-A1.
XX
PD 25-JUL-2002.
XX
PF 30-MAR-2001; 2001US-0821803.
XX
PR 30-MAR-2000; 2000US-193268P.
XX
PA (CITY ) CITY OF HOPE.
XX
PI Pfelfer GP, Dammann R;
XX
DR WPI; 2002-690479/74.
DR P-PSDB; ABG71312.
XX
PT Novel tumor suppressor gene, termed RASSFL, useful for the diagnosis of
PT predisposition to cancer by analyzing its methylation status,
PT heterozygosity or mutation
XX
PS Claim 3; Page -; 57Pp; English.
XX
CC The invention relates to an isolated tumour suppressor gene coding for

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CC splice variant RASSFL.A, RASSFL.B or RASSFL.C protein or its complement,
CC or a DNA molecule which hybridises under stringent conditions to them.
CC Also included are naturally occurring mutants of RASSFL.A, detecting (M1)
CC a methylated RASSFL gene, non-expressed RASSFL gene or an alteration in
CC RASSFL where the methylation, non-expression or alteration is associated
CC with cancer in a human, by analysing an RASSFL gene or an RASSFL gene
CC expression product from a tissue or body fluid of the human;
CC administering RASSFL agonists to treat cancer, a RASSFL non-human
CC transgenic animal, a cell line from the transgenic animal, and
CC screening for cancer therapeutics/drug candidates useful in treating
CC cancer resulting from a methylated or a mutation in RASSFL.
CC (M1) is useful for detecting methylated RASSFL gene, which is
CC useful for determining whether a human subject has or is at risk for
CC developing cancer. The method involves detecting the methylation or
CC non-expression of the gene or the presence or absence of a genetic
CC polymorphism as in the RASSFL gene of the subject, where the
CC methylation or non-expression or the presence of the genetic
CC polymorphism identifies a subject that has or is at risk for developing
CC cancer. The mutants are useful for screening for drug candidates useful
CC in treating cancer resulting from the RASSFL gene. Analysis of the RASSFL
CC gene is useful in the diagnosis of predisposition to cancer, including
CC lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
CC association between the RASSFL gene and cancer permits the early
CC presymptomatic screening of individuals to identify those at risk for
CC developing cancer. RASSFL protein is useful for identifying agonists of
CC the biological function of an RASSFL protein. RASSFL, its encoding
CC nucleic acids, antibodies and compounds identified by the screening
CC assays are useful for treating cancer. The gene for RASSFL is located
CC on chromosome 3p21.3. The present sequence encodes a natural variant of
CC RASSFL splice variant RASSFL.A.
CC Note: The present sequence is not shown in the specification but
CC was created by the indexer using the information in claim 3 and the
CC RASSFL.A sequence appearing as ABSS5574.
XX
SQ Sequence 1873 BP; 395 A; 516 C; 584 G; 378 T; 0 other;
Query Match 86.6%; Score 1455; DB 24; Length 1873;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 15; Indels 2; Gaps 1;
OY 190 GCCGCCGCCGACACGACGAGACCTGTGAGTGGGAGACCTGACCTTTCAGCAAGCA 249
DB 380 GCGGACACGAAACGAGACGAGCTGTGATGGAGACACTGACCTTTTCAGCTGA 439
OY 250 GATTGAGCAGAAATCAAGAGTCAATCAATCCAGATCAACAGCAACCTTCATGAGCTT 309
DB 440 GATTGAGCAGAAATCAAGAGTCAATCAATCCAGATCAACAGCAACCTTCATGAGCTT 499
OY 310 GAACAAGAGCGCTTCTTACACAGCTTCATCAAGTTCAGTGAAGCTGGGCCCTGT 369
DB 500 GAACAAGAGCGCTTCTTACACAGCTTCATCAAGTTCAGTGAAGCTGGGCCCTGT 559
OY 370 CTCTGTGCCCTTCACAGCAAGAACCCCTCTTCAGAGATCCCGCGGGGCCAGAGACG 429
DB 560 CTCTGTGCCCTTCACAGCAAGAACCCCTCTTCAGAGATCCCGCGGGGCCAGAGACG 619
OY 430 GGGCACAAGTGTCAAGGGCCGCACTTCTTTTACCTGGCCCAAGATGCTGTCAAGCACT 489
DB 620 GGGCACAAGTGTCAAGGGCCGCACTTCTTTTACCTGGCCCAAGATGCTGTCAAGCACT 679
OY 490 GCATGTGCTGCACGACCAAGGGGACGTAAGTATGAGGCGCTGTGCAAGTCTT 549
DB 680 ACATGTGCTGCACGACCAAGGGGACGTAAGTATGAGGCGCTGTGCAAGTCTT 739
OY 550 GGTGTGATGATGACCCCGCAGATTTGACACTTTTGGACGCGCTGAGCTCAGGCCAAGT 609
DB 740 GGTGTGATGATGACCCCGCAGATTTGACACTTTTGGACGCGCTGAGCTCAGGCCAAGT 799
OY 610 GTACTTGCAGAACTGTTGATGATGAGCAGACCCCTCGGCTGGCGCTCTGCGAGGGCC 669
DB 800 GTACTTGCAGAACTGTTGATGATGAGCAGACCCCTCGGCTGGCGCTCTGCGAGGGCC 859
OY 670 CAGTGACAAGGCCCTGAGCTTTGTCTGAAAGAAATGACTCTGGGAGGTGAACCTGGGA 729

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Db      ||| 860 CAGTGAACAAGCCCTGAGCTTTGCTCTGAGAGAAAATGACTCTGGGAGGTAACTACGGGA 919
Oy      ||| 730 CGCCTTCAGCATGCTGAGACTACATTAATCTTCTAGTATCTGACGCGGAGAGAGAGA 789
Db      ||| 920 CGCCTTCAGCATGCTGAGACTACATTAATCTTCTAGTATCTGACGCGGAGAGAGAGA 979
Oy      ||| 790 GCACCTCCGCGCAGATCTGCGAGAGTACTCTATTGCGCGCAGAAAGATCCAAAGAGCCCT 849
Db      ||| 980 GCACCTCCGCGCAGATCTGCGAGAGTACTCTATTGCGCGCAGAAAGATCCAAAGAGCCCT 1039
Oy      ||| 850 GCACCTCCGCGCGCTGGGTGACCTCTTGTACCCCAAGTGGAAAGCACAACAGCAGGCGAG 909
Db      ||| 1040 GCACGCTGCCCCCTTGGGTGACCTCTTGTACCCCAAGTGGAAAGCACAACAGCAGGCGAG 1099
Oy      ||| 910 CGCCTTCAGCATGCTGAGACTACATTAATCTTCTAGTATCTGACGCGGAGAGAGAGA 969
Db      ||| 1100 CGCCTTCAGCATGCTGAGACTACATTAATCTTCTAGTATCTGACGCGGAGAGAGAGA 1159
Oy      ||| 970 TGGAGGCGCTCTGCTGCTGGGGAATGAGCCCAAGAGAGAGTACCTTGTCTCTG 1029
Db      ||| 1160 TGGAGGCGCTCTGCTGCTGGGGAATGAGCCCAAGAGAGTACCTTGTCTCTG 1219
Oy      ||| 1030 TGTCCACCTATGAGGCTGAGCAGATGAGCTCTGCAACCCCTCTGCTTACTTGTGGCC 1089
Db      ||| 1220 TGTCCACCTATGAGGCTGAGCAGATGAGCTCTGCAACCCCTCTGCTTACTTGTGGCC 1279
Oy      ||| 1090 TTAGTGGGCGCAGGCTGAGCAGATGAGCTCTGCAACCCCTCTGCAACCCCTCTGCAAC 1149
Db      ||| 1280 TTAGTGGGCGCAGGCTGAGCAGATGAGCTCTGCAACCCCTCTGCAACCCCTCTGCAAC 1339
Oy      ||| 1150 AGAAGTCTCTCAATTTTGTCTCAGAAAGTAAATCTTGAAGACCCCTGCAACAGACACA 1209
Db      ||| 1340 AGAAGTCTCTCAATTTTGTCTCAGAAAGTAAATCTTGAAGACCCCTGCAACAGACACA 1399
Oy      ||| 1210 GGGTATGTTTGCAGGCGTGAAGGCGCCCTATCTATGAGAGAAAGCTTTTGGATCTTGAAG 1269
Db      ||| 1400 GGGTATGTTTGCAGGCGTGAAGGCGCCCTATCTATGAGAGAAAGCTTTTGGATCTTGAAG 1459
Oy      ||| 1270 TGGTCTCAGAGATATCTTATCAGAGCTAAAGGTGGTGTCTCAGAAATGAAGCAGCATTA 1329
Db      ||| 1460 TGGTCTCAGAGATATCTTATCAGAGCTAAAGGTGGTGTCTCAGAAATGAAGCAGCATTA 1519
Oy      ||| 1330 GGAAGAGTCTTGTCTCTCTACAGTGCACCACTCTCTACACACCTCTGAGTCCAGGAGT 1389
Db      ||| 1520 GGAAGAGTCTTGTCTCTCTACAGTGCACCACTCTCTACACACCTCTGAGTCCAGGAGT 1579
Oy      ||| 1390 GGTGCTCAGTATACAGATGAGCTTATGCTTCTATGAGAGAGATGCTCTGAGGCGCA 1449
Db      ||| 1580 GGTGCTCAGTATACAGATGAGCTTATGCTTCTATGAGAGAGATGCTCTGAGGCGCA 1639
Oy      ||| 1450 GGTGCTGCTGATGATGAGCTGAGCAGTTCATACCTTATTTTCTATCAAAAGCAG 1509
Db      ||| 1640 GGTGCTGCTGATGATGAGCTGAGCAGTTCATACCTTATTTTCTATCAAAAGCAG 1699
Oy      ||| 1510 GGTCTCTCCCTCAGCTGTTTTTATGAAAGTGGCGTGAAGTATGTAATGCTGGTGGCTC 1569
Db      ||| 1700 GGTCTCTCCCTCAGCTGTTTTTATGAAAGTGGCGTGAAGTATGTAATGCTGGTGGCTC 1759
Oy      ||| 1570 AGCTGAATGCTCCTGCTGGGGAAGGCTTTGGGCTGACAGTATCATCAGG--CTGCGGG 1627
Db      ||| 1760 AGCTGAATGCTCCTGCTGGGGAAGGCTTTGGGCTGACAGTATCATCAGG--CTGCGGG 1819
Oy      ||| 1628 CTGAGAGATGCTCCTCAATTAAGATTTCAAGATCCAAAAAAGAGAGAGAGAGAGAGAG 1680
Db      ||| 1820 CTGAGAGATGCTCCTCAATTAAGATTTCAAGATCCAAAAAAGAGAGAGAGAGAGAGAG 1872

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RESULT 7
 ABS55594
 ID ABS55594 standard; cDNA; 1873 BP.
 XX
 AC ABS55594;

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XX 19-DEC-2002 (first entry)
DT Human cDNA encoding tumour suppressor RASSF1.A variant 4.
XX
DE Human: ss; gene; tumour suppressor; RASSF1.A; cancer; breast cancer;
XX SNP; single nucleotide polymorphism; DNA methylation; lung cancer;
XX kidney cancer; ovarian cancer; head and neck cancer; melanoma;
XX chromosome 3p21.3.
OS Homo sapiens.
FH
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FT CDS 39..1061
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FT /product= "RASSF1.A"
FT variation
FT replace (99,C)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT replace (1044,G)
FT /*tag= c
PN US2002098530-A1.
XX
XX 25-JUL-2002.
PD
XX
XX 30-MAR-2001; 2001US-0821803.
PF
XX
XX 30-MAR-2000; 2000US-193268P.
PR
XX
XX (CITY ) CITY OF HOPE.
PA
XX
XX Pfeiffer GP, Dammann R;
XX
XX MPI: 2002-690479/74.
XX P-PSDB: ABG71313.
DR
XX
XX Novel tumor suppressor gene, termed RASSF1, useful for the diagnosis of
PT predisposition to cancer by analyzing its methylation status,
XX heterozygosity or mutation
XX
XX Claim 3; page -: 57pp; English.
XX
XX The invention relates to an isolated tumour suppressor gene coding for
XX splice variant RASSF1.A, RASSF1.B or RASSF1.C protein or its complement,
XX or a DNA molecule which hybridises under stringent conditions to them.
XX Also included are naturally occurring mutants of RASSF1.A, detecting (M1)
XX a methylated RASSF1 gene, non-expressed RASSF1 gene or an alteration in
XX RASSF1 where the methylation, non-expression or alteration is associated
XX with cancer in a human, by analysing an RASSF1 gene or an RASSF gene
XX expression product from a tissue or body fluid of the human;
XX administering RASSF1 agonists to treat cancer, a RASSF1 non-human
XX transgenic animal, a cell line from the transgenic animal, and
XX screening for cancer therapeutics/drug candidates useful in treating
XX cancer resulting from a methylated or a mutation in RASSF1.
XX (M1) is useful for detecting methylated RASSF1 gene, which is
XX useful for determining whether a human subject has or is at risk for
XX developing cancer. The method involves detecting the methylation or
XX non-expression of the gene or the presence or absence of a genetic
XX polymorphism as in the RASSF1 gene of the subject, where the
XX methylation or non-expression or the presence of the genetic
XX polymorphism identifies a subject that has or is at risk for developing
XX cancer. The mutants are useful for screening for drug candidates useful
XX in treating cancer resulting from the RASSF1 gene. Analysis of the RASSF1
XX gene is useful in the diagnosis of predisposition to cancer, including
XX lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
XX association between the RASSF1 gene and cancer permits the early
XX presymptomatic screening of individuals to identify those at risk for
XX developing cancer. RASSF1 protein is useful for identifying agonists of
XX the biological function of an RASSF1 protein. RASSF1, its encoding
XX nucleic acids, antibodies and compounds identified by the screening
XX assays are useful for treating cancer. The gene for RASSF1 is located
XX on chromosome 3p21.3. The present sequence encodes a natural variant of

```


CC RASFL1 splice variant RASFL1.A.
 CC Note: The present sequence is not shown in the specification but
 CC was created by the indexer using the information in claim 3 and the
 CC RASFL1.A sequence appearing as AB555574.
 XX
 XX
 S0 Sequence 1873 BP: 395 A; 516 C; 584 G; 378 T; 0 other:

Query Match 86.6%; Score 1455; DB 24; Length 1873;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1476; Conservative 0; Mismatches 15; Indels 2; Gaps 1;

OY 190 GCCCGCCGCGGACCGACGAGCCTGTGAGTGGAGACCTGACCTTTCTCAAGCTGA 249
 DB 380 GCGGAGACGACGACGTGACGAGCCTGTGAGTGGAGACCTGACCTTTCTCAAGCTGA 439
 OY 250 GATTGAGCAGAAATCAAGAGTACAAATGCCAGATCAACAGCAACCTTTCATGAGCTT 309
 DB 440 GATTGAGCAGAAATCAAGAGTACAAATGCCAGATCAACAGCAACCTTTCATGAGCTT 499
 OY 310 GAACAGAGAGGCTTCTACACAGGCTTCATCAAGGTTCAAGCTGAGAGCTGCGCCCTGT 369
 DB 500 GAACAGAGAGGCTTCTACACAGGCTTCATCAAGGTTCAAGCTGAGAGCTGCGCCCTGT 559
 OY 370 CTGTGCGCCCTCCAGCAAGACCCCTCTTGAGAGATGCCGGGGGGCCAGAGAG 429
 DB 560 CTGTGCGCCCTCCAGCAAGACCCCTCTTGAGAGATGCCGGGGGGCCAGAGAG 619
 OY 430 GGGCACAAGTGTACAGGCGCCGACCTTCTTTTACCTGCGCAAGATGCTGTCAAGCAGCT 489
 DB 620 GGGCACAAGTGTACAGGCGCCGACCTTCTTTTACCTGCGCAAGATGCTGTCAAGCAGCT 679
 OY 490 GCATGTGCTGTACAGCAGCAGAGGAGCAGTGAAGTATGAGGCGCTGCTGCAAAAGTCTT 549
 DB 680 ACATGTGCTGTACAGCAGCAGAGGAGCAGTGAAGTATGAGGCGCTGCTGCAAAAGTCTT 739
 OY 550 GGTGTGATGATACCCCGCAGATTTGACACTTTTGAGAGGCGCTGAGGCTGACGGCAGAT 609
 DB 740 GGTGTGATGATACCCCGCAGATTTGACACTTTTGAGAGGCGCTGAGGCTGACGGCAGAT 799
 OY 610 GTACTTCCGAGAGCTGTTGATGATGAGCAGACCCCTGCGGCTGCTGCGCAGGCGC 669
 DB 800 GTACTTCCGAGAGCTGTTGATGATGAGCAGACCCCTGCGGCTGCTGCGCAGGCGC 859
 OY 670 CAGTGACAAAGGCGCTGAGCTTGTCTGAGAGAAATGACCTGTGGAGAGTGAAGTGGGA 729
 DB 860 CAGTGACAAAGGCGCTGAGCTTGTCTGAGAGAAATGACCTGTGGAGAGTGAAGTGGGA 919
 OY 730 CGCCTTACAGTGCCTGAACTAATTAATCTTCTGATCTGACAGCGGAGAGAGAGA 789
 DB 920 CGCCTTACAGTGCCTGAACTAATTAATCTTCTGATCTGACAGCGGAGAGAGAGA 979
 OY 790 GCACCTCCGCGCAGATCTGACAGAGTACTCTATTTGCGCGCAGAGATCCAAGAGGCGCT 849
 DB 980 GCACCTCCGCGCAGATCTGACAGAGTACTCTATTTGCGCGCAGAGATCCAAGAGGCGCT 1039
 OY 850 GCAGGCGCTCCGCGCTTGGGAGTACTCTGTAACCCCGCAGTGGAGAGAGAGAGAGAG 909
 DB 1040 GCAGGCGCTCCGCGCTTGGGAGTACTCTGTAACCCCGCAGTGGAGAGAGAGAGAGAG 1099
 OY 910 CGCCAAAGTGGGCTGCTGTGAGTGTGACAGGAGCGAGTGGGCGCTGTGGAATGATGTGCA 969
 DB 1100 CGCCAAAGTGGGCTGCTGTGAGTGTGACAGGAGCGAGTGGGCGCTGTGGAATGATGTGCA 1159
 OY 970 TGGAGGCGCTTCTGTGCTGGGGGAATGAGCCGACAGAGAAAGAGTGTGCTGCCCTG 1029
 DB 1160 TGGAGGCGCTTCTGTGCTGGGGGAATGAGCCGACAGAGAAAGAGTGTGCTGCCCTG 1219
 OY 1030 TGTCCACCTAATGGGTGTAGCAGAGTATGGCTCTGACACCCCTGCTCATATATGAGGCC 1089
 DB 1220 TGTCCACCTAATGGGTGTAGCAGAGTATGGCTCTGACACCCCTGCTCATATATGAGGCC 1279
 OY 1090 TTAGTGGCGCAGGAGCTCCCTGAGAAAGTGTCCAGGCTGACAGAGAGTGTGCGAGAC 1149
 DB 1149 TTAGTGGCGCAGGAGCTCCCTGAGAAAGTGTCCAGGCTGACAGAGAGTGTGCGAGAC 1199

DB 1280 TTAGTGGCGCAGGAGCTCCCTGAGAAAGTGTCCAGGCGCTGACAGAGAGTGTGCGAGAC 1339
 OY 1150 AGAAGTCTCTCAATTTTGTCTCAGAGTGAATAATCTTGGAGACCTGCAACAGAGACA 1209
 DB 1340 AGAAGTCTCTCAATTTTGTCTCAGAGTGAATAATCTTGGAGACCTGCAACAGAGACA 1399
 OY 1210 GGGTCATGTTTGCAGGGGTGACGGGCTCATCTATGAGAAAGTTTGGATCTTGAATG 1269
 DB 1400 GGGTCATGTTTGCAGGGGTGACGGGCTCATCTATGAGAAAGTTTGGATCTTGAATG 1459
 OY 1270 TGGTCTCAGATATCCCTTATACAGAGCTAAGGCTGGCTCTAGAAATAGCAGCAGATGA 1329
 DB 1460 TGGTCTCAGATATCCCTTATACAGAGCTAAGGCTGGCTCTAGAAATAGCAGCAGATGA 1519
 OY 1330 GGAAGAGCTTGGTCTCTCTACAGTGCACAACTCTCAGACACCCCTGAGGTGAGGAGT 1389
 DB 1520 GGAAGAGCTTGGTCTCTCTACAGTGCACAACTCTCAGACACCCCTGAGGTGAGGAGT 1579
 OY 1390 GCTGGCTCAGATACAGCATGTGCTTAAATGCTTCAATATGAGAGAGATGTCCCTGGGCCA 1449
 DB 1580 GCTGGCTCAGATACAGCATGTGCTTAAATGCTTCAATATGAGAGAGATGTCCCTGGGCCA 1639
 OY 1450 GGGTCTGTAATGTGGGCACTGCGCCAGGTTCAATACCTTATTTGCTAATCAAAAGCCAG 1509
 DB 1640 GGGTCTGTAATGTGGGCACTGCGCCAGGTTCAATACCTTATTTGCTAATCAAAAGCCAG 1699
 OY 1510 GGTCTCTCCCTCAGAGTGTGTTTATGAAAGTCCGTAATGTATGTAATGTGTGGGCGCTC 1569
 DB 1700 GGTCTCTCCCTCAGAGTGTGTTTATGAAAGTCCGTAATGTATGTAATGTGTGGGCGCTC 1759
 OY 1570 AGCTGAATGCTCTCTGTGGGAAAGGGGTGGGTGACAGTCAATCAGG--CCTGGGG 1627
 DB 1760 AGCTGAATGCTCTCTGTGGGAAAGGGGTGGGTGACAGTCAATCAGG--CCTGGGG 1819
 OY 1628 CTGAGAGAAATGGCTCAATAAAGATTCAAGATCAAAAAAAGAAAAA 1680
 DB 1820 CTGAGAGAAATGGCTCAATAAAGATTCAAGATCAAAAAAAGAAAAA 1872

RESULT 8
 ABS55575
 ID ABS55575 standard; cDNA: 1664 BP.
 AC ABS55575;
 DT 19-DEC-2002 (first entry)
 XX
 DE Human cDNA encoding tumour suppressor RASFL1.B.
 XX
 KW Human; ss; gene; tumour suppressor; RASFL1.B; cancer; breast cancer;
 KW DNA methylation; lung cancer; kidney cancer; ovarian cancer;
 KW head and neck cancer; melanoma; chromosome 3p21.3.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 282..851
 FT /tag- a
 FT /product= "RASFL1.B"
 XX
 PD 25-JUL-2002.
 XX
 PF 30-MAR-2001; 2001US-0821803.
 XX
 PR 30-MAR-2000; 2000US-193268P.
 XX
 PA (CITY) CITY OF HOPE.
 XX
 PI Pfelfer GP, Dammann R;
 XX
 DR WPI: 2002-690479/74.

Query Match	48.3%	Score 811.4	DB 24	Length 813
Best Local Similarity	99.9%	Pred. No. 2.3e-196		
Matches 812	Conservative 0	Mismatches 1	Indels 0	Gaps 0

59 ATGGGCGAGGCGGAGGCGCCCTTCCTTGCAGAAATGACCTGAGCAGCAGCAGCAGCAGTGGC 118
 1 ATGGGCGAGGCGGAGGCGCCCTTCCTTGCAGAAATGACCTGAGCAGCAGCAGCAGCAGTGGC 60

QY	119	TATGTAGGCAAGAGAGACTGGGACACTGCGAGTCTCGAGCAGTACTCTTACCCGGGCAACTCG	178
Db	61	TACTGAGCCAAAGAGACTCGGACTCGGAGCTCGAGCACTTCTACCGGGCAACTCG	120
QY	179	CTAGCTCGAGAGCCGCGCCGGGACCAAGACAGCAAGCACTGTGGAGTGGGAGACACTGACCTT	238
Db	121	CTAGCTCGAGAGCCGCGCGGGACCAAGACAGCAAGCACTGTGGAGTGGGAGACACTGACCTT	180
QY	239	TCTCAGCTGAGATTGAGCAGAAAGTCAAGGAGTACAAATGCCACAGATCAACGCACTC	298
Db	181	TTTCAAGCTGAGATTGAGCAGAAAGTCAAGGAGTACAAATGCCACAGATCAACGCACTC	240
QY	299	TTTCATAGCTTGAACAAGGAGGTTCTTACACAGGCTTCATCAAGTTCAAGGTTCAAGCTGAC	358
Db	241	TTTCATAGCTTGAACAAGGAGGTTCTTACACAGGCTTCATCAAGGTTCAAGGTTCAAGCTGAC	300
QY	359	GTGCGGCTGTCTGTGTGCCCTCGACCAAGAAAGCAACCCCTCTTGACAGATGCCGGCGG	418
Db	301	GTGCGGCTGTCTGTGTGCCCTCGACCAAGAAAGCAACCCCTCTTGAGAGATGCCGGCGG	366
QY	419	GGCCCAAGACGGGGCAAACTCTCAGGGCGCGCACTTCTTTTACCTGCCCAAGATGCT	478
Db	361	GGCCCAAGACGGGGCAAACTCTCAGGGCGCGCACTTCTTTTACCTGCCCAAGATGCT	420
QY	479	GTCACACACTGCATGTGCTGTCAAGCAAAAGGCAAGGCAAGTCAATTTGAGGGCCCTGCTG	538
Db	421	GTCACACACTGCATGTGCTGTCAAGCAAAAGGCAAGGCAAGTCAATTTGAGGGCCCTGCTG	480
QY	539	CGAAAGTTCTTGATGGTGGATGATCCCGCAAGTTTGACACTTTTGAAGCGGCTGAGCGT	598
Db	481	CGAAAGTTCTTGATGGTGGATGATCCCGCAAGTTTGACACTTTTGAAGCGGCTGAGCGT	540
QY	599	CAGGCCAAGTGTACTGTGGGAAAGCTGTTGGATGATGACAGGCCCTGCGGCTGCGCTC	658
Db	541	CAGGCCAAGTGTACTGTGGGAAAGCTGTTGGATGATGACAGGCCCTGCGGCTGCGCTC	600
QY	659	CTGGCAGGGCCCAAGTACAAAGGCCCTGAGCTTTGCTCGAAGAAATGACTGGGGAG	718
Db	601	CTGGCAGGGCCCAAGTACAAAGGCCCTGAGCTTTGCTCGAAGAAATGACTGGGGAG	660
QY	719	GTCAGCTGGAGCGCTTTCAGCATGCTGTAATCACTTAACCTTCTAGCTATCTGCAAGG	778
Db	661	GTCAGCTGGAGCGCTTTCAGCATGCTGTAATCACTTCCATAGCTATCTGCAAGG	720
QY	779	GAGGAGGAGGAGACCTCGCCAGATCCGCGAAGATCTCTATGCGCCGCAAGAGATC	838
Db	721	GAGGAGGAGGAGACCTCGCCAGATCCGCGAAGATCTCTATGCGCCGCAAGAGATC	780
QY	839	CAAGAGGCCCTGACGACCTGCCCCCTTGGGTGA	871
Db	781	CAAGAGGCCCTGACGACCTGCCCCCTTGGGTGA	813
RESULT 10			
AAZ80552			
AAZ80552	ID	AAZ80552 standard; cDNA; 640 bp.	
XX	AC	AAZ80552;	
XX	AC		
XX	DT	07-APR-2000 (first entry)	
XX	DT		
DE	DE	Human colon cancer cell line SW480 cDNA clone SEQ ID NO:636.	
XX	XX		
KW	KW	Human; gene expression product; diagnosis; tumour; colon cancer;	
KW	KW	colorectal adenocarcinoma; cell line SW480; cell proliferation;	
KW	KW	cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;	
KW	KW	hyperplasia; ds.	
XX	OS	Homo sapiens.	
XX	OS		
XX	XX	W09964576-A2.	
XX	XX		

XX Eleven novel inflammation-associated genes have been identified in
CC cDNA libraries from various tissues. The genes were selected
CC according to their coexpression with the known inflammation genes,
CC CD16, L-selectin, Src-like adapter protein, Ip-30, superoxide
CC homogenzyme subunits, alpha-1-antitrypsin, C1q-A, 5-lipoxygenase
CC activating protein and SRC family tyrosine kinase. The novel
CC polynucleotides may be used in hybridization assays to diagnose a
CC disease or condition associated with altered expression of the
CC inflammation genes. Antibodies against the genes may be useful in
CC compositions for the diagnosis and treatment of such diseases
CC associated with inflammation including rheumatoid arthritis,
CC Crohn's disease, multiple sclerosis, AIDS, diabetes mellitus,
CC asthma and allergy. Additionally the polynucleotides of the
CC invention may be used for gene therapy. The present sequence is
CC human inflammation associated cDNA #8, derived from Incyte
CC Clone 2726173.

50 Sequence 3144 BP; 820 A; 792 C; 752 G; 780 T; 0 other;

Sequence 3144 BP; 820 A; 792 C; 752 G; 780 T; 0 other;

Query Match	Score	DB	Length
14.18;	236.8;	21;	3144;

Best Local Similarity 60.6%; Pred. NO. 6.4e-50;
Matches 388; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

QY	210	AGCCCTGTGAGTGGGAGACACTGACCTTTTCTCAAGCTBAGATTTGACGAGAGATCAAGG	269
Db	172	AACCTTTGTGAGAGACACAGGCGCCGCCACACTGCAGGAGATCAAGCAGAGATGACAC	231
QY	270	AGTACAAATGCCCAGATCAACAGCAACCTCTTATGAGTGTGGAACAGACGGTCTTACA	329
Db	232	GCTACAAACGGGAGAGAAAGAACTCCCTGGCATGAAACTGATGTAAGACGGCACCCTACA	291
QY	330	CAGGCTTTATCAAGTTAAGCTGAAAGCTGTGTGCGCCCTGTCTCTGTGTGCCCTCCAGCAAG	389
Db	292	CGGGTTTTCATCAAAATGTGATCTGAAACTCCGGCGGCTGTGTGACGGGTGCTGTGGATCC	351
QY	390	AGCCACCCCTCTCTGGAGAGTGCCTGGCGGGGCCGAGGAGCGGGACAAATGTCAAGCGGC	449
Db	352	GGCCCCAATCCATCTATGTATGTGCATCAAGAGAGTGAACCTGGCGGCTTACCAGGACAGC	411
QY	450	GCACTTCTTTTACCTGTGCCCAAGATGCTGTCAAGCAACCTGCATGTGTCTGTCAAGCACA	509
Db	412	GGACATCTCTTCTTACCTGGCCCTCAGATGGCATCAAGACAGCTGCACATCACAGCACCA	471
QY	510	GGGCAACGGAAAGTCAATTGAGGCCCTGTGTGCCAAAGTCTTGTGTGTGTGATGACCCCCGA	569
Db	472	CCGTCAGTAGAGTCAATCCAGGGGGCTGTCAAGAAAGTCAATGTTGTGTGCAAAATCCCCAG	531
QY	570	AGTTTGCACCTTTTGTAGCGCGCTGAGCGTCAAGCGCCAACTGTACTTGCAGAACTTTGG	629
Db	532	AGTTTGCACCTTTTAAAGGGGATACACAAAGAACGGACAAATGCTCTTCCAGAAATCTCCA	591
QY	630	ATGATGACAGACCCCTGGCGGCTGTGGGCTCTGTGGCAGAGGCCCAAGTGAACAGCCCTGAGCT	689
Db	592	TTTGTGACCGCGCCCTCTTACCTGCGCCCTGTGTGTGTGGCTTACACAGGAGTCTCTCAACT	651
QY	690	TTGTCTCTAAGGAAATATGACTGTGGGAGGTTCAACTGGGACGCTTCAACATGCCCTGAAC	749
Db	652	TTGTCTCTAAGGAGAAATGAACTGGAGAGGTGAGTGGGATGCTTCTTCATCTCCGTGAAC	711
QY	750	TACATTAACCTCTTACGTCTCTGACAGCGGAGAGAGAGAGCACTCCGCGCAATCTCTGC	809
Db	712	TTTCAAACTTCTCTAACAATCTCTGAAAAAAGAGAGAGACAAATATCCAATGTCGAA	771
QY	810	AGAACTACTCTATTTGCGCCGACGAAGATTCAGAGGCCCT	849
Db	772	AGAACTATGACAAAGTTTAAAGCAAACTGGAGAGGCCCT	811

RESULT 14
ABX12605
ID ABX12605 standard; CDNA; 3144 BP
XX

ABX12605;
13-MAY-2003 (first entry)
cDNA encoding human Ras association domain containing protein (RADCP).
Human: ras association domain containing protein; RADCP; cytosolic;
antiinflammatory; antiallergic; antiasthmatic; immunosuppressive;
gene therapy; cell proliferative disorder; inflammatory disorder;
thymus hyperplasia; allergy; asthma; hyper eosinophilia;
toxicological study; gene; ss; Incyte number 2726173CB1.
Homo sapiens.
Key Location/Qualifiers
CDS 42..839
/*tag= a
/product= "RADCP"
/note= "Ras association domain containing protein"
US6485910-B1.
11-JUL-2000; 2000US-0614069.
26-NOV-2002.
09-FEB-1998; 98US-0023655.
18-NOV-1998; 98US-0195292.
(INCY-) INCYTE GENOMICS INC.
Walker MG, Klinger TW, Krasnow RE;
WPI: 2003-298168/29.
P-PSDB: ABG74468.
New cDNA encoding mammalian Ras associated domain containing protein,
useful for screening molecules or compounds that bind to it, and for
diagnosing and treating cell proliferative and inflammatory disorders
-
Claim 1; Column 33-36; 37pp; English.
The invention describes an isolated mammalian cDNA (I) encoding mammalian
Ras associated domain containing protein (RADCP) (II). (I) is useful for
screening a number of molecules or compounds, by combining (I) with a
number of molecules or compounds under conditions to allow specific
binding, and detecting specific binding. The molecules or compounds are
selected from aptamers, DNA molecules, RNA molecules, peptide nucleic
acids, artificial chromosome constructions, peptides, transcription
factors, enhancers, repressors and regulatory molecules. (I) and (II)
are useful for diagnosis and treatment of cell proliferative and
inflammatory disorders, particularly thymus hyperplasia, allergies,
asthma and hypersensitivity. The assay methods are useful for evaluating
the efficacy of a particular therapeutic treatment regimen in animal
studies, and in clinical trials or to monitor the treatment of an
individual patient. (I) is useful to produce transgenic cell lines or
organisms which are model systems for human cell proliferative and
inflammatory disorders. (I) is also useful for performing and monitoring
toxicological studies, clinical trials and subject/patient treatment
profiles. This sequence encodes human ras association domain containing
protein (RADCP).
Sequence 3144 BP; 820 A; 792 C; 752 G; 780 T; 0 other:

Sequence 3144 BP; 820 A; 792 C; 752 G; 780 T; 0 other;

Query Match	14.1%	Score 236.8	DB 25	length 3144
Best Local Similarity	60.6%	Pred. No. 6.4e-50		
Matches 388, Conservative	0	Mismatches 252	Indels 0	Gaps 0

OY 210 AGCGTGTGGAGTGGGAGACACTGCACCTTTCTCAAGCTGAGATTGACAGAAGATC AAG 269
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 172 AACCTGTGGAGGACACACAGCGCCGCCACACATGTCAGAGATCAAGCAAGATCGACA 231

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 02:36:27 ; Search time 4070.96 Seconds

(without alignments)
10029.942 Million cell updates/sec

Title: US-10-023-530-3

Perfect score: 1680
Sequence: 1 ccggggcggtgtgtgctgcgcgc.....ccaaaaaaaaaaaaaaaaaa 1680

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_huv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_ping:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	981.6	58.4	1201 9	AL523074
2	981.2	58.4	1201 9	AL554060
3	977.8	58.1	1000 9	AL579009
4	975.6	58.1	1046 13	BX402736

5	952.4	56.7	1201 9	AL543484	AL543484
6	918.6	54.7	1201 9	AL543447	AL543447
7	916.4	54.5	1201 9	AL554061	AL554061
8	916	54.5	1201 9	AL578918	AL578918
9	914.4	54.4	1050 13	BX344328	BX344328
10	912.8	54.3	1201 9	AL523075	AL523075
11	911.2	54.2	972 9	AL576710	AL576710
12	909.8	54.2	1144 9	AL573913	AL573913
13	896.8	53.4	1201 13	BX385986	BX385986
14	886.8	52.8	1006 9	AL553818	AL553818
15	854.8	50.9	1201 13	BX458932	BX458932
16	854.6	50.9	1126 9	AL549892	AL549892
17	845.4	50.3	920 9	AL560451	AL560451
18	838.8	49.9	1017 12	BM917709	BM917709
19	837	49.8	1054 12	BM451480	BM451480
20	829	49.3	868 12	B1916624	B1916624
21	821.2	48.9	929 13	BX408425	BX408425
22	797.8	47.5	935 9	AL581893	AL581893
23	770.4	45.9	903 13	BQ689604	BQ689604
24	768.8	45.8	784 12	B1869331	B1869331
25	768	45.7	791 13	B0616689	B0616689
26	766.6	45.6	1201 13	BX458933	BX458933
27	766	45.6	906 12	B1764046	B1764046
28	762.2	45.4	846 13	BQ438298	BQ438298
29	755.2	45.0	808 12	B1917396	B1917396
30	752	44.8	918 14	CA489873	CA489873
31	747.2	44.5	797 14	CA503126	CA503126
32	742.2	44.2	934 12	B0860247	B0860247
33	736.2	43.8	764 12	BM051740	BM051740
34	726.6	43.2	907 12	B1913734	B1913734
35	726.4	43.2	778 12	B1762901	B1762901
36	714	42.5	764 10	BG570090	BG570090
37	707.6	42.1	714 12	BM725066	BM725066
38	700	41.7	778 12	BM065590	BM065590
39	684.4	40.7	924 12	BG772022	BG772022
40	670.4	39.9	676 13	BX102498	BX102498
41	669.6	39.9	813 13	B0187947	B0187947
42	667.8	39.8	774 14	CA428454	CA428454
43	665	39.6	687 12	BM981338	BM981338
44	664.6	39.6	1015 12	BM542113	BM542113
45	659.6	39.3	691 12	BM977703	BM977703

ALIGNMENTS

RESULT 1
LOCUS AL523074 1201 bp mRNA linear EST 22-MAY-2003
DEFINITION AL523074 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC001YG10 3-PRIME, mRNA sequence.
ACCESSION AL523074
VERSION AL523074.2 GI:31041335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12786567.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2262.f FOR
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DC001B005NP1a&cluster=2262.f. Contact :
Feng Liang Email : fliang@lifeotech.com URL :

OY	672	GTGCAAGAGCCCTAGCTTTTCTCTGAAAGAAATGACTCTGGGAGGTGAACCTGGACG	731
Db	962	KTRACAAAGGCCCTAGCTTTTCTCTGAAAGAAATTAACCTCTGGGAGGTGAACCTGGACG	903
OY	732	CCTTCAGCATCCCTGAACCTACATTAACCTCCACGTAATCTCAGCGGGAGAGGAGGACG	791
Db	902	CCTTCDCGATCCCTGAACCAACATAACTCTTACGTAATCTCAGCGGGAGAGGAGGAGC	843
OY	792	ACCTCCGCGACATCCTCGACGAAGTACTCTATTGCGCGCAGAAAGATCCAAAGGCCCTGC	851
Db	842	ACCTCCGCGACATCCTCGACGAAGAACTCTATTGCGCGCAGAAAGATCCAAAGGCCCTGC	783
OY	852	ACGCGTCGCCCCCTTGGGGTGGACCTCTTGTAACCCCAAGGGGAAAGGACAGACAGGACACG	911
Db	782	ACGCGTCGCCCCCTTGGGGTGGACCTCTTGTAACCCCAAGGGGAAAGGACAGACAGGACACG	723
OY	912	CCAAGTCGCGTCCGCTGTGATGTACACAGAGGCGAGTGGGGCCCTGTGGAAATGATGTGCATG	971
Db	722	CCAAGTCGCGTCCGCTGTGATGTATACAGAGGCGAGTGGGGCCCTGTGGAAATGATGTGCATG	663
OY	972	GAGGCGCTCCTGTGCTGGGGGAATGAGCCACAGAACAGCGAAGTACCTGCTCCCTGTG	1031
Db	662	GAGGCGCTCCTGTGCTGGGGGAATGAGCCACAGAACAGCGAAGTACCTGCTCCCTGTG	603
OY	1032	TCGACCTATGGGGTGAAGCCAGGTATAGCTGTGCACCCCTGTGCCCTCATTTACTGGGCTT	109
Db	602	TCGACCTATGGGGTGAAGCCAGGTATAGCTGTGCACCCCTGTGCCCTCATTTACTGGGCTT	543
OY	1092	AGTAGGGCCAGAGGCGTCCCTGAGAAAGCTCTCAGAGCCCTGCAGACAGAGATGGTGCAGACAG	1151
Db	542	AGTAGGGCCAGAGGCGTCCCTGAGAAAGCTCTCAGAGCCCTGCAGACAGAGATGGTGCAGACAG	483
OY	1152	AAGTCTCCTCAATTTTGTCTCAGAAAGTGAATACTGTGGAGACCCCTGCAGAACAGAACAGG	1211
Db	482	AAGTCTCCTCAATTTTGTCTCAGAAAGTGAATACTGTGGAGACCCCTGCAGAACAGAACAGG	423
OY	1212	GTCATGTTTGGAGGGGTAGCGGCCCTCATCTATAGGAAAGGTTTGGATCTTGAAATGTG	1271
Db	422	GTCATGTTTGGAGGGGTAGCGGCCCTCATCTATAGGAAAGGTTTGGATCTTGAAATGTG	363
OY	1272	GTCACAGATATCCCTTATCAGAGCTAAGAGGTGGGGTGCACAAATTAAGCCAGGCATTGGAG	1331
Db	362	GTCACAGATATCCCTTATCAGAGCTAAGAGGTGGGGTGCACAAATTAAGCCAGGCATTGGAG	303
OY	1332	AAGAGTCTGGTTCCTCTACAGTGCACACTCCTCACACACCCCTGAGGTGACGGAGTGC	1391
Db	302	AAGAGTCTGGTTCCTCTACAGTGCACACTCCTCACACACCCCTGAGGTGACGGAGTGC	243
OY	1392	TGGGTCAACAGTACAGCATGTGCTTAATAGCTCATATAGAGAGGATATGCCCTGGGGCCACAG	1451
Db	242	TGGGTCAACAGTACAGCATGTGCTTAATAGCTCATATAGAGAGGATATGCCCTGGGGCCACAG	183
OY	1452	GTCGTGTGAATGTGGGCACATGGCCACAGGTTTCATACCTTATTTGCTAATCAAAGCCAGAG	1511
Db	182	GTCGTGTGAATGTGGGCACATGGCCACAGGTTTCATACCTTATTTGCTAATCAAAGCCAGAG	123
OY	1512	TCTCTCCCTCAAGGTGTATTTTATGAAGTGCCTGAATGTATGTATGTGTGTGCTGCATAG	1571
Db	122	TCTCTCCCTCAAGGTGTATTTTATGAAGTGCCTGAATGTATGTATGTGTGTGCTGCATAG	63
OY	1572	CTGAATGCTCTCTGTGGGGAAAGGGGTGGGCTGACATCTCATCAACAGGCCCTGGGGC	1628
Db	62	CTGAATGCTCTCTGTGGGGAAAGGGGTGGGTAACATCTCATCAACAGGCCCTGGGGC	6

[illegible]

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1000)
TITLE	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished On Feb 16, 2001 this sequence version replaced gi:112943631.
	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2262.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgl-bin/cluster.cgi?seq=CSODK012AE01NP1&cluster=2262.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope ID : CSODK012AE01NP1. Location/Qualifiers 1..1000
FEATURES	
SOURCE	

BASE COUNT	ORIGIN
220 a	308 c
244 g	214 t
14 others	

Query Match	58.2%;	Score 977.8;	DB 9;	Length 1000;
Best Local Similarity	97.8%;	Pred. No. 4.6e-159;		
Matches 978; Conservative	11;	Mismatches 11;	Indels 0;	Gaps 0

Oy	631	IGATGAGACGGCCCTGCGGGCTGCGGCTCTGTGGCAGGGGCCAGGTGACAAAGGGCCCTAGCTT	690
Db	1000	TGATGAGACGCCCTGCGGGCTGCGGCTCTGTGGCAGGGGCCAGGTGACAAAGGGCCCTAGCTT	941
Oy	691	TGTCCCTGAAGAAAAATGACTCTGGGGAGGTGAACCTGGCAGCCCTTCAGCATGCTGAAC	750
Db	940	TGTCCCTGAAGAAAAATGACTCTGGGGAGGTGAACCTGGCAGCCCTTCAGCATGCTGAAC	881
Oy	751	ACATPACTTCTAGCTATCTTCGCAGCGGGAGAGAGAGACACCTTCGGCAGATCTCTGCA	810
Db	880	ACATPACTTCTAGCTATCTTCGCAGCGGGAGAGAGAGACACCTTCGGCAGATCTCTGCA	821
Oy	811	GAACTACTCTATTGCGCCGCCAGAAAGATCAAGAGGCCCTGCAGCGCTGCCCCCTTGGGTG	870
Db	820	GAACTACTCTATTGCGCCGCCAGAAAGATCAAGAGGCCCTGCAGCGCTGCCCCCTTGGGTG	761
Oy	871	ACCTCTGTACCCCCAGGTGGAAGGCAGACAGCAGCGCCCAAGTGCCTGCTGTGA	930
Db	760	ACCTCTGTACCCCCAGGTGGAAGGCAGACAGCAGCGCCCAAGTGCCTGCTGTGA	701
Oy	931	GTTGTGACAGGGGCCAGTGGGGCTGTGGAAATGATGTGATGGAGGCCCTCCCTGCTCGGG	990
Db	700	GTTGTGACAGGGGCCAGTGGGGCTGTGGAAATGATGTGATGGAGGCCCTCCCTGCTCGGG	641
Oy	991	GGAATGAGCCCGAGAGAACAGGAAGTACTTGTCTCTGTGTGCACCTATGAGGTATACC	1050
Db	640	GGAATGAGCCCGAGAGAACAGGAAGTACTTGTCTCTGTGTGCACCTATGAGGTATACC	581
Oy	1051	AGGATGAGCTTCGACACCCCTCTGCCCTATTACTGTGGCCCTTAAGTGGGCCAGAGGCTGCGCT	1111
Db	580	AGGATGAGCTTCGACACCCCTCTGCCCTATTACTGTGGCCCTTAAGTGGGCCAGAGGCTGCGCT	521

FEATURES	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
LOCUS	BX402736				
DEFINITION	BX402736 Homo sapiens PLACENTA COT 25-NORMALIZED				
ACCESSION	BX402736				
KEYWORDS	BX402736.1 GI:30632100				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1. (bases 1 to 1046)				
TITLE	L. W. B., Gruber, C., Jesse, J. and Polyes, D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished				
LOCUS	BX402736	1046 bp	mRNA	linear	EST 13-MAY-2003
DEFINITION	BX402736 Homo sapiens PLACENTA COT 25-NORMALIZED				
ACCESSION	clone CS0D1081YB21 3-PRIME, mRNA sequence.				
KEYWORDS	BX402736				
SOURCE	BX402736.1 GI:30632100				
ORGANISM	EST.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1. (bases 1 to 1046)				
JOURNAL	L. W. B., Gruber, C., Jesse, J. and Polyes, D.				
COMMENT	Full-length cDNA libraries and normalization				
LOCUS	BX402736	1046 bp	mRNA	linear	EST 13-MAY-2003
DEFINITION	BX402736 Homo sapiens PLACENTA COT 25-NORMALIZED				
ACCESSION	clone CS0D1081YB21 3-PRIME, mRNA sequence.				
KEYWORDS	BX402736				
SOURCE	BX402736.1 GI:30632100				
ORGANISM	EST.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1. (bases 1 to 1046)				
JOURNAL	L. W. B., Gruber, C., Jesse, J. and Polyes, D.				
COMMENT	Full-length cDNA libraries and normalization				

Query Match	Similarity	Score	DB 13	Length	1046
Best Local	97.1%	Pred. No. 1.1e-158			
Matches	983	Conservative	13	Mismatches	15
				Indels	1
				Gaps	1
BASE COUNT	242 a	295 c	254 g	219 t	36 others
ORIGIN					
Query Match	58.1%	Score 975.6	DB 13	Length 1046	
Best Local	97.1%	Pred. No. 1.1e-158			
Matches	983	Conservative	13	Mismatches	15
				Indels	1
				Gaps	1
604	CCAACTGTA	CTGCGGAAGCTGTGGATGATGACAGCCCTCGCGCTCGGCTCTCTGC	663		
1046	CCAAGTTT	ACCTTGGGGAAGCTTTGGATGATGACAGCCCTCGCGCTCGGCTCTCTGC	987		
664	AGGCGCC	AGTGCACAAAGCCCTGAGCTTTGTCTTGAAGAAAATGACTCTGGGAGGTGA	723		
986	AGGGGCC	CAKGTGCAAGGCGCTGAGCTTTTCTCTGAAGAAAATGACTCTGGGAGGTGA	927		
724	CTGGAGC	CGCTTCACATGCGCTGACACTACATTAATCTTACGTAATCCGACGGGAGGA	783		
926	CTGGAGC	CGCTTCACATGCGCTGACACTACATTAATCTTACGTAATCCGACGGGAGGA	867		
784	GGAGAGA	CACTCTCGCCAGATCTCTCAGAAAGTACTCTTAATGCGCCAGAAAGATCCA	843		
866	GGAGAGA	CACTCTCGCCAGATCTCTCAGAAAGTACTCTTAATGCGCCAGAAAGATCCA	807		
844	GGCCCTG	CAAGCTGCGCCCTTGGGTGACCTCTTACCCCGAGGTGAAGGCAACAGC	903		
806	GGCCCTG	CAAGCTGCGCCCTTGGGTGACCTCTTACCCCGAGGTGAAGGCAACAGC	748		
904	AGGCAAG	CGCCAAAGTGCCTGTGAGTGTGACAGGGCCAGTGGGCGCTGTGAATGAG	963		
747	AGGCAAG	CGCCAAAGTGCCTGTGAGTGTGACAGGGCCAGTGGGCGCTGTGAATGAG	688		
964	TGTGATG	AGGCGCCCTTCCGTGCGTGGGGAATGACCCAGAAAGGAAGTACTTGC	1022		
687	TGTGATG	AGGCGCCCTTCCGTGCGTGGGGAATGACCCAGAAAGGAAGTACTTGC	628		
1024	TCCCTGT	TCCACCTATGATGATGACAGGTATGATGCTGACCCCTCTGACCTATTAC	1083		
627	TCCCTGT	TCCACCTATGATGATGACAGGTATGATGCTGACCCCTCTGACCTATTAC	568		
1084	TGGCGTT	AGTGGGCGAGGGCTGCCCTGAGAACTGCTCCAGAGGCTGACAGAGTGT	1143		
567	TGGCGTT	AGTGGGCGAGGGCTGCCCTGAGAACTGCTCCAGAGGCTGACAGAGTGT	508		
1144	GCAGACA	CAAGCTCTCAATTTTGTGTCAGAAATGAAAATCTTGGAGACCTTCGAAC	1203		
507	GCAGACA	CAAGCTCTCTCAATTTTGTGTCAGAAATGAAAATCTTGGAGACCTTCGAAC	448		
1204	AGAACAG	GGTATGTTGACGGGCTGACGGCCCTCATCTATGAGGAAAAGTTTGGATCT	1263		
447	AGAACAG	GGTATGTTGACGGGCTGACGGCCCTCATCTATGAGGAAAAGTTTGGATCT	388		
1264	TGAATGT	GTCTCAGAGATATCTTATACAGAGTAAAGGTTGGTCTCAGAAATGACAGG	1322		
387	TGAATGT	GTCTCAGAGATATCTTATACAGAGTAAAGGTTGGTCTCAGAAATGACAGG	328		
1324	CATTGAG	AAGAGTCTGTTTCTCTACAGTGCACCTCTCACACACCTTGAGTCA	1383		
327	CATTGAG	AAGAGTCTGTTTCTCTCTACAGTGCACCTCTCACACACCTTGAGTCA	268		
1384	GGGAGTG	TGCTGCTACAGTATGCTTATGCTTATATAGAGAGAGTCTCT	1443		
267	GGGAGTG	TGCTGCTCACAATAGCACTGCTTATGCTTATATAGAGAGAGTCTCT	208		
1444	GGGCGAG	GGTCTGTTGTAATGTGGCACTGGCCAGTTCATTAATTTTGTCTATCAA	1503		
207	GGGCGAG	GGTCTGTTGTAATGTGGCACTGGCCAGTTCATTAATTTTGTCTATCAA	148		
1504	AGCCAGG	GTCTCCCTCAGGTGTTTATGAAGTGCATTAATGATGTGTGT	1563		

Db 147 AGCCAGAGTCTCTCCCTCAGGTGTTTATGATGAGTGAATGTATGTGTGT 88

QY 1564 GGCCTCAGCTGATGATGCTCTCTGTTGGGAGAAAGGTTGGGTGACAGTCA 1615
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 Db 87 GGCCTCAGCTGATGATGCTCTCTGTTGGGAGAAAGGTTGGNTTACATCATCA 36

RESULT 5
 AL543484
 LOCUS
 DEFINITION AL543484 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1003YK08 5-PRIME, mRNA sequence.
 AL543484
 VERSION AL543484.2 GI:31265331
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced g1:12875962.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2262.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1003BF04P1&cluster=2262.f. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1003BF04P1.

FEATURES
 source
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1003YK08"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 266 a 263 c 338 g 283 t 51 others

ORIGIN

Query Match 56.7% Score 952.4; DB 9; Length 1201;
 Best Local Similarity 97.2% Pred. No. 1e-154;
 Matches 962; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 691 TGTCTGAGAGAAATGATCTGGGGAGGTGAAGTGGAGCGCTTCAGCATGCTGA 750
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 Db 66 TGTCTGAGAGAAATGATCTGGGGAGGTGAAGTGGAGCGCTTCAGCATGCTGA 125

QY 751 ACATTAATCTCTAATGATCTGACAGGGAGAGAGACACCTCCGCCAGATCTGCA 810
 |||||
 Db 126 ACATTAATCTCTAATGATCTGACAGGGAGAGAGACACCTCCGCCAGATCTGCA 185

QY 811 GAAGTCTCTTAATGATCTGACAGGGAGAGAGACACCTCCGCCAGATCTGCA 870
 |||||
 Db 186 GAAGTCTCTTAATGATCTGACAGGGAGAGAGACACCTCCGCCAGATCTGCA 245

QY 871 ACCTCTTGTACCCAGGTGAGAGGAGACAGACAGCGCCCAAGTGGTGGCTGTGA 930
 |||||
 Db 246 ACCTCTTGTACCCAGGTGAGAGGAGACAGACAGCGCCCAAGTGGTGGCTGTGA 305

QY 931 GTGTGACAGGCGCAGTGGGCGCTGTGAGATGAGTGTGATGAGAGCCCTCTGTGG 990
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Db 306 GTGTGACAGGCGCAGTGGGCGCTGTGAGATGAGTGTGATGAGAGCCCTCTGTGG 365

QY 991 GGAATAGGCCAGAGAGAAAGCGAATAGCTGTGCTCCCTGTCACCTAATGAGTGA 1050
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 Db 366 GGAATAGGCCAGAGAGAAAGCGAATAGCTGTGCTCCCTGTCACCTAATGAGTGA 425

QY 1051 AGGTATGGCTGTGACACCCCTGTGCTCTTACTTGGGCTTGTGAGGCGCAGGCT 1110
 |||||
 Db 426 AGGTATGGCTGTGACACCCCTGTGCTCTTACTTGGGCTTGTGAGGCGCAGGCT 485

QY 1111 GAGAACCTCTCCAGGCTGTGACAGAGAGTGTGACAGAGAGTCTCTCAATTTTGT 1170
 |||||
 Db 486 GAGAACCTCTCCAGGCTGTGACAGAGAGTGTGACAGAGAGTCTCTCAATTTTGT 545

QY 1171 CTCAGAGTGAATAATTTGTGAGAGCCCTGCAACAGAGAGGTCATGTTTGCAGGGTGA 1230
 |||||
 Db 546 CTCAGAGTGAATAATTTGTGAGAGCCCTGCAACAGAGAGGTCATGTTTGCAGGGTGA 605

QY 1231 CGGCCCTCATATGAGAGAAAGGTTTGGATCTTGAATGTGTCTCAGATATCTTATC 1290
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 Db 606 CGGCCCTCATATGAGAGAAAGTCTTGGATCTTGAATGTGTCTCAGATATCTTATC 665

QY 1291 AGAGCTAAGGCTGGTGTCTCAGATATAGGAGGATTTGAGAGAAAGTCTTGTCTCTC 1350
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 Db 666 AGAGCTAAGGCTGGTGTCTCAGATATAGGAGGATTTGAGAGAAAGTCTTGTCTCTC 725

QY 1351 TACAGTGAACCTCTCACACACCCGAGGTCAGGAGTGTGCTGACAGTACAGCATG 1410
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 Db 726 TACAGTGAACCTCTCACACACCCGAGGTCAGGAGTGTGCTGACAGTACAGCATG 785

QY 1411 TGCCTTAATGCTTCATATGAGAGAGATGTCCCTGAGGCTGTGTGATGTGGGA 1470
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 Db 786 TGCCTTAATGCTTCATATGAGAGAGATGTCCCTGAGGCTGTGTGATGTGGGA 845

QY 1471 CTGGCCAGGTATATACCTTATTTGCTAATCAAGGAGGTCTCTCAGAGTGT 1530
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 Db 846 CTGGCCAGGTATATACCTTATTTGCTAATCAAGGAGGTCTCTCAGAGTGT 905

QY 1531 TTATGAGTGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1590
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 Db 906 TTATGAGTGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 965

QY 1591 AAAGGGTGGGTGACAGTATCATCAGGCTGGGGCTGAGAGAAATTTGGCTAATAAG 1650
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 Db 966 AAAGGGTGGGTGACAGTATCATCAGGCTGGGGCTGAGAGAAATTTGGCTAATAAG 1025

QY 1651 ATTTCAGATCCAAAAA 1680
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 Db 1026 TTATGATCCCTCAAAAAA 1055

RESULT 6
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 LOCUS AL543447 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1003YK08 3-PRIME, mRNA sequence.
 AL543447
 DEFINITION AL543447.2 GI:31265294
 ACCESSION
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced g1:12875925.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2262.f. For more information about this cluster, see

<http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq=CSOD1003BF04NP1cluster=2262.f>. Contact : Feng liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/InvitrogenCorporation1600> Faraday Avenue Genoscope sequence ID : CSOD1003BF04NP1.

FEATURES

source

Location/Qualifiers

1. 1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOD1003YK08"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 269 a 303 c 275 g 268 t 86 others

ORIGIN

Query Match 54.7%; Score 918.6; DB 9; Length 1201;
 Best Local Similarity 97.3%; Pred. No. 7.1e-149;
 Matches 926; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

691 TGTCTTGAAGAAATGACTCTGGGAGAGTGAATCGGACGCTTACAGATCCTGAAC 750
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 954 TGTCTTGAAGAAATGACTCTGGGAGAGTGAATCGGACGCTTACAGATCCTGAAC 895
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 894 ACATTAATCTTCTAGCTATCTGACAGCGGAGAGAGGACGCTCCGCGAGATCCTGMA 835
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 811 GAAGTACTCTTAATGCGCGCAGAAAGATCCAAAGAGGCGCTGACGCGCTCCCTTGGGTG 870
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 834 GAAGTACTCTTAATGCGCGCAGAAAGATCCAAAGAGGCGCTGACGCGCTCCCTTGGGTG 775
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 871 ACCTCTTGTACCCCGAGGTGGAAGGACACAGCAGGCGCCGCAAGTCCGTCGCTGTGA 930
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 774 ACCTCTTGTACCCCGAGGTGGAAGGACACAGCAGGCGCCGCAAGTCCGTCGCTGTGA 715
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 714 GTGTGACAGGCGCAGTGGGCGCTGTGAATGAGTGTGATGAGGCGCTCCCTGTCGTGG 655
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 991 GGAATGAGCCGAGAGAACAGGAGTACCTGCTCCCTGTGTCCACCTATGAGGTGTACC 1050
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 594 AGATATGGCTCTGCACCCCTCTGCCCTTACTATGAGGCGCTTAAGTGGCCAGGCGCT 535
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 1111 GAGAAGTGTCTCCAGGCGCTGCAGAGAGTGTGCAGACAGAGTCTCTCAATTTTGT 1170
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 534 GAGAAGTGTCTCCAGGCGCTGCAGAGAGTGTGCAGACAGAGTCTCTCAATTTTAT 475
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 1171 CTGCAAGTGAATACTTTGAGACCTGTGCAGAGAACAGAGGCTATGTTTCAGGGGTGA 1230
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 474 CTCGAGAGTGAATACTTTGAGACCTGTGCAGAGAACAGAGGCTATGTTTCAGGGGTGA 415
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 1231 CGGCGCTCATATGAGAGAAAGTTTGGATCTTGAATGTGGTCTCAGAGATTCCTTATC 1290
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 414 CGGCGCTCATATGAGAGAAAGTTTGGATCTTGAATGTGGTCTCAGAGATTCCTTATC 355
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 1291 AGAGCTAAGGGTGGGTGCTCAGATTAAGGCGAGGATTAAGAGAGTCTTGGTTCTCTC 1350
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 354 AGAGCTAAGGGTGGGTGCTCAGATTAAGGCGAGGATTAAGAGAGTCTTGGTTCTCTC 295
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 1351 TACAGTGCAACTCTCTACACACCCCTGAGTCAAGGAGTGTGGCTCACAATACAGATG 1410
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 294 TACAGTGCAACTCTCTACACACCCCTGAGTCAAGGAGTGTGGCTCACAATACAGATG 235
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 DB 224 TGCCTTAATGCTTCAATGAGAGAGATGTCCTGGGCGAGGCTCTGTGTAATGTGGCA 175
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 DB 114 TTATGAAGTGGCTGAATGATATGATGTGTGTGCTCAGCTGAATGCTTCCTGTGGG 55
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 DB 54 AAAGGGTGGGCTGACATCATATCAGGCGATGAGGCGCTGAGAGATTTGGCT 3

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 LOCUS AL554061 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CSOD1081YB21 5-PRIME, mRNA sequence.
 ACCESSION AL554061
 VERSION AL554061.2 GI:31275874
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessup, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12894483.
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2262.f. For
 more information about this cluster, see
<http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq=CSOD1081YB21>
 Faraday Avenue Genoscope sequence ID : CSOD1081YB21.
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 /organism="Homo sapiens"
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 /clone="CSOD1081YB21"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 250 a 330 c 356 g 230 t 35 others
 ORIGIN

Query Match 54.5%; Score 916.4; DB 9; Length 1201;
 Best Local Similarity 92.0%; Pred. No. 1.7e-148;
 Matches 997; Conservative 30; Mismatches 49; Indels 8; Gaps 6;

QY 1 CCGGGGCGGTGTTGGGCTACGAGCGGAGACTGGGGACGGGCGGTACGGCTAT 60
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 DB 121 CCGGGGCGGTGTTGGGCTACGAGCGGAGACTGGGGACGGGCGGTACGGCTAT 180
 |||||
 QY 61 GGGGAGGCGGAGGCGGCTTTTGAATGACCTGAGAGCGAGCAGCAGACATGCTGA 120
 |||||
 DB 181 GGGGAGGCGGAGGCGGCTTTTGAATGACCTGAGAGCGAGCAGCAGACATGCTGA 240
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OY 121 CTGACGCCAAGAGACTCGGAGCTCGAGAGTACTTACCGCGCAACTCGCT 180
    |||||
DB 241 CTGACGCCAAGAGACTCGGAGCTCGAGAGTACTTACCGCGCAACTCGCT 300
OY 181 ACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
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DB 301 ACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
OY 241 TCAAGCTGATTTGAGCAGAAATGATCAAGAGTACATGCGCGAGTCAAGAACCTCTT 300
    |||||
DB 361 TCAAGCTGATTTGAGCAGAAATGATCAAGAGTACATGCGCGAGTCAAGAACCTCTT 420
OY 301 CATGAGCTTGAACAAGAGAGCTTTCTTACAGAGCTTCAATCAAGTTCAAGCTGAGTGT 360
    |||||
DB 421 CATGAGCTTGAACAAGAGAGCTTTCTTACAGAGCTTCAATCAAGTTCAAGCTGAGTGT 480
OY 361 GCGCCCTGTCTGTGCGCTTCCAGCAAGAGCGCGCGCGCGCGCGCGCGCG 420
    |||||
DB 481 GCGCCCTGTCTGTGCGCTTCCAGCAAGAGCGCGCGCGCGCGCGCGCGCG 540
OY 421 CCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
    |||||
DB 541 CCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
OY 481 CAAGCACTGATGTGCTGTACGCAAGAGCGCGCGCGCGCGCGCGCGCGCG 540
    |||||
DB 601 CAAGCACTGATGTGCTGTACGCAAGAGCGCGCGCGCGCGCGCGCGCGCG 659
OY 541 AAAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
    |||||
DB 660 AAAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 719
OY 601 CGGCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 659
    |||||
DB 720 CGGCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 779
OY 660 TGGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
    |||||
DB 780 TGGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 839
OY 720 TGAATCTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 779
    |||||
DB 840 TGAATCTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 899
OY 780 ACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
    |||||
DB 900 ACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
OY 840 AAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 898
    |||||
DB 960 AAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1019
OY 899 AAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 958
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DB 1020 AAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1079
OY 959 ATGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018
    |||||
DB 1080 ATGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
OY 1019 CTGCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078
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DB 1137 CTGCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
OY 1079 ATTA 1082
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DB 1195 ATKD 1198

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RESULT 8
LOCUS AL578918/c 1201 bp mRNA linear EST 01-JUN-2003

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DEFINITION AL578918 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
ACCESSION CDNA clone CS0DK005YK06 3-PRIME, mRNA sequence.
VERSION AL578918.2 GI:31317106
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 1201)
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
On Feb 16, 2001 this sequence version replaced gi:12943453.
Contact: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 Evry cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2262.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK005BF03NP1&cluster=2262.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DK005BF03NP1.
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK005YK06"
/cell_type="HELA"
/clone_11b="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 263 a 354 c 261 g 243 t 80 others
ORIGIN

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Query Match 54.5%; Score 916; DB 9; Length 1201;
Best Local Similarity 97.2%; Pred. No. 2e-148;
Matches 955; Conservative 7; Mismatches 18; Indels 3; Gaps 3;
OY 631 TGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
    |||||
DB 1022 TGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964
OY 691 TGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
    |||||
DB 963 TGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 905
OY 751 ACATTAATCTCTACGATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
    |||||
DB 904 ACATTAATCTCTACGATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 845
OY 811 GAAGTACTCTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 869
    |||||
DB 844 GAAGTACTCTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 785
OY 870 GACCTCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 929
    |||||
DB 784 GACCTCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 725
OY 930 AGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 989
    |||||
DB 724 AGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
OY 990 GGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1049
    |||||
DB 664 GGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605

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QY 1050 CAGGTATGCTCTGTGACACCCCTCTGCTCATTTACTGGGCTTTAGTGGCCAGGGCTGCC 1109
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 Db 604 CAGGTATGCTCTGTGACACCCCTCTGCTCATTTACTGGGCTTTAGTGGCCAGGGCTGCC 545
 |||||||
 QY 1110 TGAGAGGCTGCTCCAGGCTGACAGAGAGTGTGACAGACAGATCTCCCAATTTTGTG 1169
 |||||||
 Db 544 TGAGAGGCTGCTCCAGGCTGACAGAGAGTGTGACAGACAGATCTCCCAATTTTGTG 485
 |||||||
 QY 1170 TCTCAGAGAGTGAATCTTTGAGACCCCTGCAACAGAACAGAGTCTATTTGACAGGGGTG 1229
 |||||||
 Db 484 TCTCAGAGAGTGAATCTTTGAGACCCCTGCAACAGAACAGAGTCTATTTGACAGGGGTG 425
 |||||||
 QY 1230 ACGGCCCCATCTATGAGAGAAAGTTTGGATCTTGAATGTGTCTCAGCATATCTTTAT 1289
 |||||||
 Db 424 ACGGCCCCATCTATGAGAGAAAGTTTGGATCTTGAATGTGTCTCAGCATATCTTTAT 365
 |||||||
 QY 1290 CAGAGCTAAGGGTGGGTCTCAGAAATAAGCAGGCAATGAGAGAGCTTGGTTTCT 1349
 |||||||
 Db 364 CAGAGCTAAGGGTGGGTCTCAGAAATAAGCAGGCAATGAGAGAGCTTGGTTTCT 305
 |||||||
 QY 1350 CTACAGTGCACACTCTCTCACACACCCCTGAGGTGAGGAGTCTGCTCACAGTACAGCAT 1409
 |||||||
 Db 304 CTACAGTGCACACTCTCTCACACACCCCTGAGGTGAGGAGTCTGCTCACAGTACAGCAT 245
 |||||||
 QY 1410 GTGCTTAATGCTTCATATGAGAGAGATGCTCCCTGGGCGAGGCTCTGTGAATGTGGGC 1469
 |||||||
 Db 244 GTGCTTAATGCTTCATATGAGAGAGATGCTCCCTGGGCGAGGCTCTGTGAATGTGGGC 185
 |||||||
 QY 1470 ACTGCCCCAGGTTCATACCTTATTTGGTAATCAAAAGCCAGGCTCTCCCTCAGAGTGT 1529
 |||||||
 Db 184 ACTGCCCCAGGTTCATACCTTATTTGGTAATCAAAAGCCAGGCTCTCCCTCAGAGTGT 125
 |||||||
 QY 1530 TTTATGAAGTCCGTGAATGTAATGTGTGTGGTCCCTCAGTGAATGCTCTGTGGG 1589
 |||||||
 Db 124 TTTATGAAGTCCGTGAATGTAATGTGTGTGGTCCCTCAGTGAATGCTCTGTGGG 65
 |||||||
 QY 1590 GAAAGGGGTGGGTGACAGTCA 1612
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 Db 64 GAAAGGGGTGGGTGACAGTCA 42
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RESULT 9 1050 bp mRNA linear EST 01-MAY-2003
 BX344328
 LOCUS BX344328 Homo sapiens PLACENTA COT 25-NORMALIZED Homo. sapiens cDNA
 DEFINITION clone CSOD1081YB21 5-PRIME, mRNA sequence.
 ACCESSION BX344328
 VERSION 1 GI:30309092
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1050)
 L.I.M.B., Gruber, C., Jesse, J. and Polayres, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2262.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSIA1021ZB10P1
 cluster=2262.f. Contact : Feng Liang Email : fliang@lifetech.com
 URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSIA1021ZB10P1.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="CSOD1081YB21"
 /issue="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 228 a 302 c 328 g 186 t 6 others
 ORIGIN
 Query Match 54.4%; Score 914.4; DB 13; Length 1050;
 Best Local Similarity 99.2%; Pred. No. 3.9e-148;
 Matches 923; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
 1 CCGGGGGGCTGTTGGGCGGCTACGAGCGGAGAGCTGGGGAGCGGGGTATCGGCTAT 60
 121 CCGGGGGGCTGTTGGGCGGCTACGAGCGGAGAGCTGGGGAGCGGGGTATCGGCTAT 180
 QY 61 GGGCGAGGCGGAGCGGCTTCTTTCGAAATGACCTGACAGCAGCAGCAGTGGCTA 120
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 Db 181 GGGCGAGGCGGAGCGGCTTCTTTCGAAATGACCTGACAGCAGCAGCAGTGGCTA 240
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 QY 121 CTGAGCCAAAGAGACTGCGACTGCGAGCTGAGCAGTCTCAACCGCGCAACTGGCT 180
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 Db 241 CTGAGCCAAAGAGACTGCGACTGCGAGCTGAGCAGTCTCAACCGCGCAACTGGCT 300
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 QY 181 AGCTCGAGGCGGCGGCGGAGCAGAGCAGCAGCTGTGGAGTGGAGACACTGACCTTTC 240
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 Db 301 AGCTCGAGGCGGCGGCGGAGCAGAGCAGCAGCTGTGGAGTGGAGACACTGACCTTTC 360
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 QY 241 TCAAGCTGACATTTAGCAGAAATGATCAAGAGTACATATGCCAGATCAACAGCAACTCT 300
 |||||||
 Db 361 TCAAGCTGACATTTAGCAGAAATGATCAAGAGTACATATGCCAGATCAACAGCAACTCT 420
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 QY 301 CATGAGCTGTAACAAGAGAGGCTTCTTACAGAGCTTATCAAGTTTCAAGTGAAGCTGT 360
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 Db 421 CATGAGCTGTAACAAGAGAGGCTTCTTACAGAGCTTATCAAGTTTCAAGTGAAGCTGT 480
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 QY 361 GCGGCTGTCTCTGTGCTCCCTCCAGCAAGAACCCACCTCTTGGAGATGCGCGGGG 420
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 Db 481 GCGGCTGTCTCTGTGCTCCCTCCAGCAAGAACCCACCTCTTGGAGATGCGCGGGG 540
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 QY 421 CCCAGAGCGGGGCAAGTGTACAGGCGCGGCACTTCTTTTACCTGCCCAGAGTGTGT 480
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 Db 541 CCCAGAGCGGGGCAAGTGTACAGGCGCGGCACTTCTTTTACCTGCCCAGAGTGTGT 600
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 QY 481 CAAGCACCCTGATGTGCTGTCAGCAGCAGAGGGCAGTGAAGTCAATTGAGGCCCTGCTGG 540
 |||||||
 Db 601 CAAGCACCCTGATGTGCTGTCAGCAGCAGAGGGCAGTGAAGTCAATTGAGGCCCTGCTGG 660
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 QY 541 AAAGTTCTTGTGTGATGATGACCCCGCAAGTTTGCATCTTTGAGGCGCGTGAAGCTCA 600
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 QY 601 CGGCGAAGTGTACTTGGGGAAGCTGTGATGATGAGACAGCCCTGCGGCTGCTCT 660
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 Db 721 CGGCGAAGTGTACTTGGGGAAGCTGTGATGATGAGACAGCCCTGCGGCTGCTCT 780
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 Db 781 GGCAGGGCCCAAGTACAGGCGGCTGAGCTTGTGCTTAAGAAATGACTGTGGGAGGT 840
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 QY 721 GAAGTGGGAGCCTTTCAGATGCTGTAATCAATTAATCTTCTAGTATCTCTGACGCGGA 780
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 Db 841 GAAGTGGGAGCCTTTCAGATGCTGTAATCAATTAATCTTCTAGTATCTCTGACGCGGA 900
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 QY 781 GGAGGAGAGACACTCCGCGAGATCTGCGAAGTACTCTATTGCGCGCAAGATCA 840
 |||||||
 Db 901 GGAGGAGAGACACTCCGCGAGATCTGCGAAGTACTCTATTGCGCGCAAGATCA 960
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 QY 841 AGAGGCGCTGACAGGCGGCGGCTTGGGTGACCTCTTGTATACCCCAAGTGAAGCGAGAC 900
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Db 961 AGAGCCCTGACACGCTTGGTGGTACCTTTGTA-CCCCAGGTGGAAGCAGAM 1019

Qy 901 AGACGACGACCCCAAGTCGTGCTGCTGA 930
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Db 1020 ARACGACGACGCMAGTGGTGGCTGTGA 1049

RESULT 10
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LOCUS AL523075 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DC001G10 5-PRIME, mRNA sequence.
ACCESSION AL523075
VERSION AL523075.2 GI:31041336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12786568.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2262.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC001BD05QPL&cluster=2262.f. Contact :
Feng Liang Email: fliang@life.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC001BD05QPL.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_11b="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 271 a 325 c 355 g 219 t 31 others

ORIGIN

Query Match 54.3%; Score 912.8; DB 9; Length 1201;
Best Local Similarity 98.2%; Pred. No. 7,1e-148;
Matches 951; Conservative 3; Mismatches 10; Indels 4; Gaps 3;

Qy 1 CCGGGGGCGGTGTGGCGGTACGACGCGGAGCTGGGGGCGGGGTACGGCTAT 60
Db 102 CCGGGGGCGGTGTGGCGGTACGACGCGGAGCTGGGGGCGGGGTACGGCTAT 161
Qy 61 GGGCGAGCGGAGGGGCGCTTCTTTCGAATGACC-TGGAGCAGCAGCAGCAGTGGCT 119
Db 162 GGGCGAGCGGAGGGGCGCTTCTTTCGAATGACATGGAGCAGCAGCAGCAGTGGCT 221
Qy 120 ACTGACGCAAGAGACTCGACTCGAGCTGAGCAGTACACTTACCGCGGCAACCTGC 179
Db 222 ACTGACGCAAGAGACTCGACTCGAGCTGAGCAGTACACTTACCGCGGCAACCTGC 281
Qy 180 TAGCTGCGAGCGCGCGCGG-GACCAGAGCAGCCTGTGTGAGTGGAGAGACCTGACTT 238
Db 282 TAGCTGCGAGCGCGCGCGGNGACAGCAGCCTGTGTGAGTGGAGAGACCTGACTT 341
Qy 239 TCTCAAGCTGAGATTTGAGCAGAGATCAAGAGTACATGCCCATCATCAAGCAACCTC 298
|||||

Db 342 TCTCAAGCTGAGATTTGAGCAGAGATCAAGAGTACATGCCCATCATCAAGCAACCTC 401

Qy 299 TCTCATGAGCTTGAACAGAGCGTTCTTTCACAGGCTTTCATCAAGTTTCAAGTGAAGCTG 358
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Db 402 TCTCATGAGCTTGAACAGAGCGTTCTTTCACAGGCTTTCATCAAGTTTCAAGTGAAGCTG 461

Qy 359 GTGGCGCTGTCTGTGTGCGCTTCACAGCAAGAAAGCCCTCTTCAGAGATCCCGCGCG 418
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Db 462 GTGGCGCTGTCTGTGTGCGCTTCACAGCAAGAAAGCCCTCTTCAGAGATCCCGCGCG 521

Qy 419 GGGCCAGAGCGGGGCGCAGAGTGTACAGGCGCCGACCTCTCTTTACTGCGCCAGAGATGT 478
|||||

Db 522 GGGCCAGAGCGGGGCGCAGAGTGTACAGGCGCCGACCTCTCTTTACTGCGCCAGAGATGT 581

Qy 479 GTCAAGCACCTGCATGTGCTGTACAGCAGCAAGGGGCGAGTGAATGAGGCGCCGTGC 538
Db 582 GTCAAGCACCTGCATGTGCTGTACAGCAGCAAGGGGCGAGTGAATGAGGCGCCGTGC 641

Qy 539 CGAAGTTCTTGTGTGTGTGATGACCCCGCAAGTTTGACCTTTGAGGCGCGTGAAGCT 598
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Db 642 CGAAGTTCTTGTGTGTGTGATGACCCCGCAAGTTTGACCTTTGAGGCGCGTGAAGCT 701

Qy 599 CACGGCCAAAGTACTTGTGCGGAAGCTGTGATGATGACAGCCCTGCGGCTGC 658
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Db 702 CACGGCCAAAGTACTTGTGCGGAAGCTGTGATGATGACAGCCCTGCGGCTGC 761

Qy 659 CTGGCAGGCGCCAGTGACAGAGCCCTGACCTTTGCTTGAAGAAATGACTGTGGGAG 718
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Db 762 CTGGCAGGCGCCAGTGACAGAGCCCTGACCTTTGCTTGAAGAAATGACTGTGGGAG 821

Qy 719 GTGAAGTGGAGCGCTTCAGATGCTGATACATATCTTCTGATCTGTCGACGG 778
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Db 822 GTGAAGTGGAGCGCTTCAGATGCTGATACATATCTTCTGATCTGTCGACGG 881

Qy 779 GAGGAGGAGAGACACTCCGCGCAGATCTGCAAGTACTCTATTTGCCCGCAAGAGATC 838
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Db 882 GAGGAGGAGAGACACTCCGCGCAGATCTGCAAGTACTCTATTTGCCCGCAAGAGATC 941

Qy 839 CAAAGAGCCCTGACAGCCCTGCGCCCTTGGGTGACCTCTGTATACCCCAAGTGAAGGAC 898
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Db 942 CAAAGAGCCCTGACAGCCCTGCGCCCTTGGGTGATCTGTATACCCCAAGTGAAGGAC 1001

Qy 899 ACAGCAGGACGCGCAAGTGTGCTGCGGTGATGATGACAGGCGCAGTGGGCTGTGGA 958
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Db 1002 AAAGCAGGACGCGCAAGTGTGCTGCGGTGATGATGATGATGATGATGATGATGAT 1059

Qy 959 ATGAGTGT 966
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Db 1060 ATGAGTGT 1067

RESULT 11
AL576710/c 972 bp mRNA linear EST 01-JUN-2003
LOCUS AL576710 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1077YN05 3-PRIME, mRNA sequence.
ACCESSION AL576710
VERSION AL576710.2 GI:31314991
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 972)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12939121.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2262.f. For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1077CG03NP1&cluster=2262.f>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0D1077CG03NP1.

FEATURES

Source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1077YN05"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      231 a      293 c      228 g      205 t      15 others
ORIGIN

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Query Match 54.2%: Score 911.2; DB 9; Length 972;

Best Local Similarity 97.6%: Pred. No. 1.4e-147; Matches 944; Conservative 8; Mismatches 12; Indels 3; Gaps 3;

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967 TTGTCTCTGAAGG-AAATGACTCTGGGGA-GTGAATCTGGAGCGCTTCAGCATCCTGAA 910
749 CTACATTAATCTTCCAGTATCCCTGACGCGGAGAGAGAGAGACACCTCCGCAATCTCTG 808
909 CTACATTAATCTTCCAGTATCCCTGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850
809 CAGAACTACTCTTATCTCCGCGAGAAATGATCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
849 CAGAACTACTCTTATCTCCGCGAGAAATGATCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
869 TGACCTTTTATACCCCGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
789 TGACCTTTTATACCCCGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730
929 GAGTGTACAGAGGCGCAATGAGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATG 988
729 GAGTGTACAGAGGCGCAATGAGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATG 670
989 GGGGAATGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048
669 GGGGAATGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 610
1049 CCAAGTATGAGCTGTGACACCCCTGTGCTTATTAAGTGGCCCTTAAGTGGCCCTTAAGTGG 1108
609 CCAAGTATGAGCTGTGACACCCCTGTGCTTATTAAGTGGCCCTTAAGTGGCCCTTAAGTGG 550
1109 CTGAGAGAGAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1168
549 CTGAGAGAGAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 490
1169 GTCTCAGAAAGTGAAGATCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1228
489 GTCTCAGAAAGTGAAGATCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
1229 GACGGCCCTCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1288
429 GACGGCCCTCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 370
1289 TCAGAGAGTAAAGGGGTGCTCAGAAATGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1348
369 TCAGAGTAAAGGGGTGCTCAGAAATGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 310
1349 TCACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1408
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OY 1409 TGTGCTTAATGCTTCAATATGAGAGAGAGATGTCCTGGGCGCAGGGCTGTGTGAATGTGG 1468
DB 249 TGTGCTTAATGCTTCAATATGAGAGAGATGTCCTGGGCGCAGGGCTGTGTGAATGTGG 190
OY 1469 CACGTGGCCAGGCTTCAATACCTTATTTGCTAATCAAGGAGAGAGAGAGAGAGAGAGAG 1528
DB 189 CACGTGGCCAGGCTTCAATACCTTATTTGCTAATCAAGGAGAGAGAGAGAGAGAGAGAG 130
OY 1529 TTTATGAGAGGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1588
DB 129 TTTATGAGAGGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 70
OY 1589 GGAAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1647
DB 69 GGAAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10
OY 1648 AAGATTT 1654
DB 9 WTKWTTT 3

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RESULT 12

AL573913/c 1144 bp mRNA linear EST 31-MAY-2003

DEFINITION AL573913 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

ACCESSION AL573913

VERSION AL573913.2 GI:31295249

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1144)

AUTHORS I. M. B., Gruber, C., Jessee, J. and Polayres, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 16, 2001 this sequence version replaced g1:12933608.

Contact: Genoscope

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2262.f. For

more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1054BF03NP1&cluster=2262.f>

Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0D1054BF03NP1.

Location/Qualifiers

1. 1144

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="CS0D1054YK06"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 262 a 317 c 289 g 219 t 57 others

Query Match 54.2%: Score 909.8; DB 9; Length 1144;

Best Local Similarity 95.0%: Pred. No. 2.4e-147; Matches 959; Conservative 18; Mismatches 24; Indels 8; Gaps 4;

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OY 626 TTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 685
DB 1010 TTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 952

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OY	686	AGCTTTTGTCCGGAAGAAAATGACTCTGTGGGAGGTGAACCTGGACGCTTTAGCATGCTT	745
Db	951	AGCTTTTGTCCGGAAGAAAATGACTCTGTGGGAGGTGAACCTGGACGCTTTAGCATGCTT	893
OY	746	GAACACATTAACCTTCCTACGTATTCCTGCAGCGGGGAGGAGGAGGACATCTCCGCAGATC	805
Db	892	GTACTACTAATCTTCTACTTATATCTGCAGCGGGGAGGAGGAGGACATCTCCGCAGATC	833
OY	806	CTGCAGAAAGTACTCTATTTGCGCCGAGAAAGATCCAAAGAGGCCCTGCACGCCCTGCCCTT	865
Db	832	CTGCAGAAAGTACTCTATTTGCGCCGAGAAAGATCCAAAGAGGCCCTGCACGCCCTGCCCTT	773
OY	866	GGGTGACCTCTTTGTATACCCCAAGGTGTGAAGGCAGACAGCAGCAGCCCAAGTGGTCCG	925
Db	772	GGGTGACCTCTTTGTATACCCCAAGGTGTGAAGGCAGACAGCAGCAGCCCAAGTGGTCCG	713
OY	926	TGTAGATGTGACAGGGGACGATGGGGCCCTGTGGAATGATGTGTGCATGTGAGGGCCCTCCTGTG	985
Db	712	TGTAGATGTGACAGGGGACGATGGGGCCCTGTGGAATGATGTGTGCATGTGAGGGCCCTCCTGTG	653
OY	986	CTGGGGGAATGAGCCCAAGAGAACGGAAGTAGCTTGCTCCCTGTGTCACCTATAGGTG	1045
Db	652	CTGGGGGAATGAGCCCAAGAGAACGGAAGTAGCTTGCTCCCTGTGTCACCTATAGGTG	593
OY	1046	TAGCAGAGTATGGCTCTGCACCCCTCCTGCTCCCTCAATTAATGGGCCCTTAATGGCCACAGGCT	1105
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OY	1106	GCCCTGAGAACTGCTCCAGGCTCTGCACAGAGAGTGTGCACAGCAGAAATGTCTCCCAATT	1165
Db	532	GCCCTGAGAACTGCTCCAGGCTCTGCACAGAGAGTGTGCACAGCAGAAATGTCTCCCAATT	473
OY	1166	TTTGTCTCAGAAATGAAATTTTGGAGACCTCGCAACAGAACAGGCTCATGTTTGCAGG	1225
Db	472	TTTGTCTCAGAAATGAAATTTTGGAGACCTCGCAACAGAACAGGCTCATGTTTGCAGG	413
OY	1226	GGTGACGGCCCTCAATCTATGAGGAAAGGTTTTGGATCTTGAATGGTCTCAGATATATCC	1285
Db	412	GGTGACGGCCCTCAATCTATGAGGAAAGGTTTTGGATCTTGAATGGTCTCAGATATATCC	353
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Db	352	TTATTCAGAGCTAAGGGTGGGTGCTCAGAAATTAAGCAGGCAATTGAGGAAGACTCTGTGTTT	293
OY	1346	CTCTCTACAGTGCACACTCTCACAACACCTGAGGTGAGGAGTGTGGTCTCACAGTACA	1405
Db	292	CTCTCTACAGTGCACACTCTCACAACACCTGAGGTGAGGAGTGTGGTCTCACAGTACA	233
OY	1406	GCATGTGCTTAATGCTTCATATAGAGAGAAATGCCCGGGCCAGAGGCTCTGTGCAATGT	1465
Db	232	GCATGTGCTTAATGCTTCATATAGAGAGAAATGCCCGGGCCAGAGGCTCTGTGCAATGT	173
OY	1466	GGGCACTGGCCAGGTTTCATACCTTATTTGGCTA-----ATCAAAGCCAGGGTCTCTCCCT	1520
Db	172	GGGCACTGGCCAGGTTTCATACCTTATTTGGCTA-----ATCAAAGCCAGGGTCTCTCCCT	113
OY	1521	CAGGTGTTTTTTAT--GAAGTGGCGTAATGTATGTAATGTGTGTGGGCTCAGCTGAATGC	1579
Db	112	CAGGTGTTTTTTATCGAAGTCCGTGAATGTATGTAATGTGTGTGGGCTCAGCTGAATGC	53
OY	1580	CTCCGTTGGGAAAAGGGTTGGGGGAGCAGATCATCATAGGCGCTGGGGC 1628	
Db	52	CTCCTGTGGGAAAGGGTTGGGGTGTGCTGTCATCATCAGGCGTGGGGC 4	
RESULT 13			
BX385986/c			
LOCUS			
DEFINITION			
BX385986 Homo sapiens PLACENR1A cont 25-NORMALIZED Homo sapiens cDNA			
clone CS001025YB05 3-PRIME, mRNA sequence.			
BX385986			
ACCESSION			
BX385986.1 GI:30436712			
VERSION			

Db	553	GGGCGAGGGGCGCCCTGAGAGCTGCTCCAGAGCCCTGCAGCAGGAGTGGTGCAGACGAAG	494
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Db	493	TCCTCCTAATTTTTGTCTCAGAAATGAAATCTTGGAGACCCCTGCAACACAGACAGGGTC	434
QY	1215	ATGTTTCAGAGGGGAGCGGCCCTCATCTATGAGGAAAGTTTGGATCTTGATATGGTTC	1274
Db	433	ATGTTTCAGAGGGGAGCGGCCCTCATCTATGAGGAAAGTTTGGATCTTGATATGGTTC	374
QY	1275	TCAGGATATCCTTATCAGAGCTAAAGGTTGGTGTCTCAGAAATTAAGCAGGACTTGAGAAAG	1334
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QY	1335	AGCTTGGTTCTCTCAAGTGGCACTCCTCACACCCCTGAGTCAAGGAGTGTCTGG	1394
Db	313	AGCTTGGTTCTCTCAAGTGGCACTCCTCACACCCCTGAGTCAAGGAGTGTCTGG	254
QY	1395	CTCACAATACAGCATGTGCTTAATGCTTCATTAAGAGAGGATGCCCTGGGCCAGGGTC	1454
Db	253	CTCACAATACAGCATGTGCTTAATGCTTCATTAAGAGAGGATGCCCTGGGCCAGGGTC	194
QY	1455	TGTTGTAATGTGGGCACTGGGCCAGAGTTTCATACCTTAATTTGCTATCAAAAGCAGGGCT	1514
Db	193	TGTTGTAATGTGGGCACTGGGCCAGAGTTTCATACCTTAATTTGCTATCAAAAGCAGGGCT	134
QY	1515	CTCCCTCAGGTGTTTTTAATGAATGCGTGAATGTATGTATGTGTGGCTGCACCTG	1574
Db	133	CTCCCTCAGGTGTTTTTAATGAATGCGTGAATGTATGTATGTGTGTGSSCCYCAVCTG	74
QY	1575	AATGCTCTCTGTGGGGAAGGGGTTGGGGTACACGTCA	1612
Db	73	AATGCTCTCTGTGGGGAAGGGGTTGGGGTGTGTCG	36

FEATURES	source
LOCUS	AL553818
DEFINITION	1006 bp mRNA linear EST 31-MAY-2003
ACCESSION	AL553818 Homo sapiens PLAECENTRA COT 25-NORMALIZED Homo sapiens CDNA
VERSION	AL553818
KEYWORDS	AL553818.2 GI:1275632
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1. (bases 1 to 1006)
COMMENT	Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization unpublished On Feb 15, 2001 this sequence version replaced gi:12894009. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqrest@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2262.f For more information about this cluster, see http://www.genoscope.cns.fr/ cg1-bin/cluster.cgi?seq=CS0D1077CG03QPlac1cluster=2262.f. Contact : Peng Liang Email : liang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paradey Avenue Genoscope ID : CS0D1077CG03QPl.
	Location/Qualifiers 1..1006

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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313 g	189 t
4 others	

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Best Local Similarity	98.9%	Pred. No. 2,36-143		
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QY 62	GGCGAGGCGGAGGCGCTTCTTTCGAATATGACTCGTAGACACAGACAGACAGTGGCTAC	121		
DB 68	GGGGAGGCGGAGGCGCTTCTTTCGAATATGACTCGTAGACACAGACAGACAGTGGCTAC	127		
QY 122	TGCAGCCAGAGAGACTCGGACTCGGAGGCTCGACAGATCACTTACCCGGCGCACTCGGCA	181		
DB 128	TGCAGCCAGAGAGACTCGGACTCGGAGGCTCGACAGATCACTTACCCGGCGCACTCGGCA	187		
QY 182	GCTCGAGGCGCGCGCGGGAGCCAGACAGAGCCCTGTGAGTGGAGACACTGTACTTCT	241		
DB 188	GCTCGAGGCGCGCGCGGGAGCCAGACAGAGCCCTGTGAGTGGAGACACTGTACTTCT	247		
QY 242	CAAGCTGAGATTGACACAAATATCAAGATATCAATCCAGATCAACAGCAACTCTTC	301		
DB 248	CAAGCTGAGATTGACACAAATATCAAGATATCAATCCAGATCAACAGCAACTCTTC	307		
QY 302	ATGAGCTTGAAACAAGAGAGGTTCTTACACAGCTTTCATCAAGTTCAGCTGAAGCTGGTG	361		
DB 308	ATGAGCTTGAAACAAGAGAGGTTCTTACACAGCTTTCATCAAGTTCAGCTGAAGCTGGTG	367		
QY 362	CGCGCTGTCTGTGCGCTCCAGACAGAGAGCCACCTCTTGCAGATGCGCGGGGCG	421		
DB 368	CGCGCTGTCTGTGCGCTCCAGACAGAGAGCCACCTCTTGCAGATGCGCGGGGCG	427		
QY 422	CCAGAGCGGGGACAAATGTACAGGGCGGCGACTTCTTTACGTGCCCAAGATGCTGTTC	481		
DB 428	CCAGAGCGGGGACAAATGTACAGGGCGGCGACTTCTTTACGTGCCCAAGATGCTGTTC	487		
QY 482	AAGCAGCTGATGTGCTGTCAAGCACAAGGGGACAGTATCATTTGAGGCCCTGTCCGA	541		
DB 488	AAGCAGCTGATGTGCTGTCAAGCACAAGGGGACAGTATCATTTGAGGCCCTGTCCGA	547		
QY 542	AAGTCTTGATGATGATGACCCCGCAAGTTTCATCTTTAAGGCGCGTGAAGCTCAC	601		
DB 548	AAGTCTTGATGATGATGACCCCGCAAGTTTCATCTTTAAGGCGCGTGAAGCTCAC	607		
QY 602	GGCAGATGTACTTCCGAGAACTGTTGGATATGACAGCCCTGGGGCTGACGACTCG	661		
DB 608	GGCAGATGTACTTCCGAGAACTGTTGGATATGACAGCCCTGGGGCTGACGACTCG	667		
QY 662	GCAGGGGCCAGTGAAGAAGGCCCTGAGCTTTCCTGAAGAAATGACTCTGGGGAGGTG	721		
DB 668	GCAGGGGCCAGTGAAGAAGGCCCTGAGCTTTCCTGAAGAAATGACTCTGGGGAGGTG	727		
QY 722	AAGTGGGAGGCTTACAGATGCTGAACTATCAATCTTCTAGCTATCTCGAGCGGGAG	781		
DB 728	AAGTGGGAGGCTTACAGATGCTGAACTATCAATCTTCTAGCTATCTCGAGCGGGAG	786		
QY 782	GAGGAGGAGACCTTCGCGCAGATCCTGACGAAGTACTCTATTGCCGCCAAGATCCAA	841		
DB 787	GAGGAGGAGACCTTCGCGCAGATCCTGACGAAGTACTCTATTGCCGCCAAGATCCAA	846		
QY 842	GAGGCCCTGCAAGCCCTGCGCCCTTGGGTGACCTTGTACCCCAAGTGGAGGACAGACA	901		
DB 847	GAGGCCCTGCAAGCCCTGCGCCCTTGGGTGACCTTGTGTACCCCAAGTGGAGGACAGACA	906		
QY 902	GCAGGACAGGCGCAATGCGTGCCTGTGAGTGTACAGGGCGACGTGGGGCGTGGGAATG	961		
DB 907	GCAGGACAGGCGCAATGCGTGCCTGTGTGAGTGTACAGGGCGACGTGGGGCGTGGGAATG	964		
QY 962	AATGTGATGAGAGGCCCTCTGTGCTGGGGGA	993		


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Db 133 CTGCACCCCTTGGCCCTTATTACTGCGCTTATGTCGCGCCAGGCTGCCCTGAGAACTGC 192
Qy 1121 TCAGAGCCCTGCAGAGAGAGTGTGTGCAGACAGAACTCTCAATTTTGTCTCAGAACTG 1180
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Db 253 AAAATCTTGGAGACCCCTGCAGACAGAGGCTCATGTTTGCAGGGGTGCAGGCCCTCAT 312
Qy 1241 CTATGAGAAAGTTTGTGATCTTGAATGTGTCTCAGAGATATCCTTATCAGAGTAAG 1300
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Db 313 CTATGAGAAAGTTTGTGATCTTGAATGTGTCTCAGAGATATCCTTATCAGAGTAAG 372
Qy 1301 GTGGGTCTCAGAAATAGGAGGCA-TTGAGAAAGAGTCTTGTTCTCTCTACAGTCC 1359
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Db 373 GTGGGTCTCAGAAATAGGAGGCAATTTGANGAAAAATCTTGTTCTCTCTTACAGTCC 432
Qy 1360 AACTCTCAGACACCCCTGAGGTCAAGGAGTGTCTGCTACA 1400
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RESULT 2

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US-09-614-069-2
: Sequence 2, Application US/09614069
: Patent No. 6485910
: GENERAL INFORMATION:
: APPLICANT: Walker, Michael G.
: APPLICANT: Klingner, Tod M.
: APPLICANT: Krasnow, Randi E.
: TITLE OF INVENTION: RAS ASSOCIATION DOMAIN CONTAINING PROTEIN
: FILE REFERENCE: PC-0014 CIP
: CURRENT FILING DATE: US/09/614, 069
: PRIOR FILING DATE: 2000-07-11
: PRIOR APPLICATION NUMBER: 09/023,655
: PRIOR FILING DATE: 1998-02-09
: PRIOR APPLICATION NUMBER: 09/195,292
: PRIOR FILING DATE: 1998-11-18
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PERL Program
: SEQ ID NO 2
: LENGTH: 3144
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID NO: 6485910 2726173CB1
US-09-614-069-2

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Query Match 14.1% Score 236.8; DB 4; Length 3144;
Best Local Similarity 60.6%; Pred. No. 4.6e-58;
Matches 388; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

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Qy 210 AGCCTGGAGTGGAGAGACACCTTCTCAAGCTGAGATGAGAGAAATCAAG 269
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Db 172 AACCTGGAGAGAGACACAGCGCCGCCACATGCAAGGAAATCAAGAGATGACA 231
Qy 270 AGTACAATGCCAGATCAACAGCAACTCTTCATGATGTTAAACAGAGGCTCTTACA 329
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Db 232 GCTACAACAGCGAGAGAGAACTGCTGGGCAATGAACATGAGAGAGCGACCTTACA 291
Qy 330 CAGGCTTCATCAGGTTCAAGTGAAGTGTGCGCCCTGTCTGTGCGCTTCACAGAGA 389
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Db 292 CGGTTTCAATCAAGATGATCTGAACTCCGCGGCTGTGACGCTGCTGCGATCC 351
Qy 390 AGCCACCTCTCTGAGAGATGCGGGGGGCGCCAGAGACCAAGTTCAGCGGCC 449
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Db 352 GGGCCCAAGTCCATTAATGATGCCATCAAGAGAGTGAACCTGCGGCTACACAGACAAGC 411
Qy 450 GCACTTCCTTTTACCTGCCCAAGAGATGCTGCAAGCACTGATGCTGTCAAGCAAA 509
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Db 412 GGACATCTCTTACCTGCGCCCTTATGATGCATCAAGCAAGCTGACATCAGCAGCACCA 471

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Qy 510 GGGCAGTGAATCATTTAGAGCCCTTGTGCGGAAAGTTCTGTGTGATGACCCCGCA 569
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Db 472 CCGTAGTAGAGTATTCAGAGGGGCTGCTCAAGAAATGATGTTGTGACAAATCCCGACA 531
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Qy 630 ATGATGACAGCCCGCTGCGGCTGCGGCTCTGCGAGGGCCAGTACAAAGCCCGAGCT 689
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Db 592 TTGCTGACCGCCCTTACTTACCTGCGCTGTGCTTGTGCGCTGACACAGAGTCTCAACT 651
Qy 690 TTGCTGAGAGAAATGACTCTGCGGAGTGAAGTGGAGCGCTTTCAGATGCTCTGAAC 749
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Db 652 TTGCTGAAGAGAAATGAACCTGAGAGAGTAAAGTGGATGCTTCTCAATCCCTGAAC 711
Qy 750 TACATACTTCTCTACATCTCTCTGACGCGGAGAGAGAGAGACACCTCCGCCAGATCTGC 809
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Db 712 TTCAGAACTTCTTAACAATCTCTGAAAAAGAGAGAGACAAATCCAAAGTGCAAA 771
Qy 810 AGAAGTACTCTTATGCGCCAGAGATCCAAAGAGGCCCT 849
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Db 772 AGAAGTATGACAAAGTTTAGGCAAGAAACTGAGAGGCCCTT 811

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RESULT 3

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US-08-942-572-1
: Sequence 1, Application US/08942572
: Patent No. 6140488
: GENERAL INFORMATION:
: APPLICANT: Avtuch, Joseph
: APPLICANT: Zhang, Xian-Feng
: TITLE OF INVENTION: RAS-BINDING PROTEIN
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: US
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/942,572
: FILING DATE: 01-OCT-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Fraser, Janis K.
: REGISTRATION NUMBER: 34,819
: REFERENCE/DOCKET NUMBER: 08472/737001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELERX: 200154
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3018 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 31...1269
: US-08-942-572-1

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Query Match 13.2%; Score 221.2; DB 3; Length 3018;
 Best Local Similarity 57.5%; Pred. No. 1.4e-53;
 Matches 397; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

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OY 171 GAACTCGCTAGCTGGCAGGCGCGGAGCAGAGCAGCTTGGAGTGGAGACAC 230
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DB 566 GAAAGACCTTCACCCCACTTGAACCAAGATGTGTGAAGCAGTGGAGACACAC 625
OY 231 CTGACCTTCTCAAGCTGAGATTGAGCAGAAATCAAGAGATACAGCCAGATCAACA 290
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DB 626 ACCGCCCAAGATACAGAGATCAAGCAGAGATGACAGCTATACAGCAGAGAGAAC 685
OY 291 GCACCTCTTCAAGCTTGAACAAGAGAGCTTTCACAGAGCTTTCATCAAGGTTTCAAC 350
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DB 686 ACTGCTGGCATGAAGCTGAGTGAAGATGGCAGCTACACAGGTTTCATCAAGAGCAT 745
OY 351 TGAACCTGTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 410
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DB 746 TGAACCTCGAGCGGCGAGTGAAGGTCGCTGAGTCCGCGCCAGTCCATCTATGAGT 805
OY 411 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 470
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DB 806 CCATTAAAGAAATGAACCTCTGACGACGACGACGACGACGACGACGACGACGACGAC 865
OY 471 AGGATGCTGTCAAGCACTGATGTCTGTCAAGCAAGAGGCGAGCTGAAGTCAATGAG 530
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DB 866 TCGATGCTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 925
OY 531 CCGCTCTGGAAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 926 GGTCTCTCAAGAAATCATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 985
OY 591 CTGACGCTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 986 TACACAAAGATGAGACAGTGTCTTCCAGAACTCTCCATTTGCTGACTTCTCTCTACC 1045
OY 651 TCGGCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1046 TTGCTCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1105
OY 711 CTGGGAGAGTGAACGCGGCTTCAAGATGCTTCAATCAATCAATCAATCAATCAATCC 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1106 CTGGAGAGGTGAGTGGATGCTTTCATTCCTGAACCTTTCATCAATCAATCAATCC 1165
OY 771 TCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1166 TGGAAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1225
OY 831 AGAAGATCCAGAGGCGGCTGACGCGCTGCC 860
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1226 AGAAACTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1255

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RESULT 4
 US-09-484-970B-23
 ; Sequence 23, Application US/09484970B
 ; Patent No. 6426186
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Karen A.
 ; APPLICANT: Volkmut, Wayne
 ; APPLICANT: Walker, Michael G.
 ; TITLE OF INVENTION: BONE REMODELING GENES
 ; FILE REFERENCE: PB-0014 US
 ; CURRENT APPLICATION NUMBER: US/09/484,970B
 ; CURRENT FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 23
 ; LENGTH: 3030
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6426186 218628.2CB1
 ; NAME/KEY: unsure
 ; LOCATION: 9, 64
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-484-970B-23

Query Match 7.8%; Score 131; DB 4; Length 3030;
 Best Local Similarity 60.1%; Pred. No. 1.4e-27;
 Matches 218; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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OY 248 GAGATTGACCAAGATCAAGAGTACAAATGCCAGATCAAGCAACCTTCAATGAGC 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 211 GAGATCAACCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAG 270
OY 308 TTGAACAAGAGGTTCTTACACAGCTTCAACAGTTCACAGTTCAGTTCAGTTCAGTTC 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 271 CTGAGTGAAGAGGCGCCTTACACAGGCTTCAAAAGTCAATCTGAAGTCCGCGGCT 330
OY 368 GTCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 GTGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 390
OY 428 CAGGCGCAAGTGTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 391 CTGGCGGCTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 450
OY 488 CTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 451 CTGACATATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 510
OY 548 TTGTGTGTGAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 511 ATGGTTGTGGAACATCCCGAAGATTGACATTTTAACCGGATACACAAGAGCGAGCA 570
OY 608 GTG 610
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DB 571 GTG 573

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RESULT 5
 US-09-614-069-4
 ; Sequence 4, Application US/09614069
 ; Patent No. 6485910
 ; GENERAL INFORMATION:
 ; APPLICANT: Walker, Michael G.
 ; APPLICANT: Klingler, Tod M.
 ; APPLICANT: Krasnow, Randi E.
 ; TITLE OF INVENTION: RAS ASSOCIATION DOMAIN CONTAINING PROTEIN
 ; FILE REFERENCE: PC-0014 CIP
 ; CURRENT APPLICATION NUMBER: US/09/614,069
 ; CURRENT FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 09/023,655
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 09/195,292
 ; PRIOR FILING DATE: 1998-11-18
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 4
 ; LENGTH: 510
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6485910 2726173P6
 ; NAME/KEY: unsure
 ; LOCATION: 338, 498, 502, 506
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-614-069-4

Query Match 3.7%; Score 62.4; DB 4; Length 510;
 Best Local Similarity 66.2%; Pred. No. 3.1e-08;
 Matches 90; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Oy	654	AGGGCCCAAGTACAGAGGCGCTGAGCTTTGTCTCTGAAGAAATAATGACTCTGTGGGAGAGTAA	723
Db	1058	CCGTAACCCGGCGTCAACCGCATCGGCGCCCTGCGGCCAGAGGGCCGACGGTGTGAGGG	1127
Oy	724	CTGGGACGCTTCAGCATGACCTGAATCATTAATCTTCCTAGTATCTCGACGGGAGGA	783
Db	1128	COTGTGGCGCGCGCGCGAGCTGTGTGATGTGGGCGCCCGCAGACGTGTGTGTGGCTGTCA	1187
Oy	784	GGAGGAGCACTCCGCCAGATCTTCGACAGACTACTCTTATTGCCGCCAGAAAGATCCAGA	843
Db	1188	GGAGGGCAGCGGACACCTGACGCTTCGCGCTTACCATTTACAGCCAGCGCAGAGAGACGG	1247
Oy	844	GGCCCTGACGCTGCGCCCTTGGGTG	870
Db	1248	TCTCAGCGCGGACACCTGCGCTG	1274

RESULT 9
US-09-252-991A-7202/c

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: Sequence 7202, Application US/0925291A
: Patent No. 6551795
:
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,91A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 7202
: LENGTH: 666
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
: US-09-252-91A-7202

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Query Match	2.4%	Score 39.6	DB 4	Length 666
Best Local Similarity	45.7%	Pred. No. 0.13		
Matches	138	Conservative	0	Mismatches 164; Indels 0; Gaps 0
QY	569	AAGTTTGACATCTTTGAGCGCGCTGAGCGTACAGGCCAAGTGTACTGCGGAAGCTGTGG	628	
Db	663	AAGGGCGTAGGCGCGCGCGCTGGCGGAGAAAGTCTCGCTGGGTAGAGCCTGGAAACCTTGAC	604	
QY	629	GATGATAGAGCAAGCCCTGCGGCTGCGGCTCCTCGGACAGGCGCCAGTGAACAAGGCTTGAGC	688	
Db	603	GATATCTGTTCCACACTGCGCCCTCGCGACACAGGACCCCTACCCGGGTACACGGCCATTCGGC	544	
QY	689	TTTGTCTCGAAGAAATGACTGTGGGAGGTGAACTGGGAGCGCTTGACGATGCTGAA	748	
Db	543	GCCCTGCGGCGAGGGGCGGATGCGGTGTCTCAGGGCGTGTGGCCCGGCGCCAGCTGTG	484	
QY	749	CTACATAACTTCTACGATCTCTGACGCGGAGGAGGAGAGCACTCCGACAGATCTG	808	
Db	483	ATGGGGGCGCGCGGAGGCTGCTGTGTGGCTGTGAGAGACGGGACGCGGACCTTAGGCTG	424	
QY	809	CAGAACTACTCTTATTTGCGGCGCAGAAGATCCAAAGAGGCGCTTGACGCTTGCCCTTGGG	868	
Db	423	CGCTTCTACATTCACGCGACGCGCAGAAAGACGGTCTCAAGCGGGGACCCACCACTGTGGC	364	
QY	869	TG 870		
Db	363	TG 362		

RESULT 10
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOVLPX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: PT29pt-F15
 US-08-232-463-14

[illegible]

Query Match 2.2%; Score 37.4; DB 4; Length 744;
Best Local Similarity 50.3%; Pred. No. 0.62;
Matches 92; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Search completed: August 20, 2003, 09:54:34
Job time : 117.3 secs

OY 561 ACCCCGCAAGTTTGACCTCTTGAGCGGCTGAGCGCCCAAGTGTACTTCGGA 620
DB 470 ATCACCCTCGCTCGCTCGTGCAGCGGATGAGATCCACACCAAGGCTCTGGCCG 529
OY 621 ACCTGTGGATGATGACAGCCCTGCGGCTGCGCTCGGAGGCGCCAGTGACAAG 680
DB 530 TGGTATGAGACCTCTCCGCTCCCTCTCTGACGACTGGCGCGAGCCAGTATGAGG 589
OY 681 CCCTGAGCTTTCCTGGAAGAAATGACTGTGGGAGGTGAATGGAGCGCTTCAGCA 740
DB 590 TCCTCACCAGCAGCAGATGTGACCGCCCTGCAGAGAGAGATCGGCAACGTCTGGCCT 649
OY 741 TGC 743
DB 650 GGC 652

RESULT 15

US-09-461-325-471
; Sequence 471, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 471
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-471

Query Match 2.2%; Score 37.4; DB 4; Length 1221;
Best Local Similarity 48.8%; Pred. No. 0.8;
Matches 101; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

OY 593 GAGCGTCACAGGCCAGTGTGCGGAGCGTGTGAGATGAGAGCCCTCGCGCTG 652
DB 802 GACCCGACACAGCGCGCTGCGCTGCGAGCTGGGAGTGGCAACCGGATGCTG 861
OY 653 CGGCTCCTGGCAGGCCAGTGACAAAGCGCTGAGCTTGTCTGGAAGAAATGACTCT 712
DB 862 CAGTTCTCGTGCACCTGGTGGCGAGAGAGCGGCTTATAGCTGACGCTCACTGACCC 921
OY 713 GGGAGGTGACTGGAGCGCTTCAGCATGCTGAACATCAATTAATTCTTACGTATCTG 772
DB 922 GTGGCCGCGCAGCTGGGCGCCACACAGCCAGCGGCTCTCCGTACCCCTTCTCC 981
OY 773 CAGCGGAGAGAGAGAGACCTCCGC 799
DB 982 ACTTGGGACAGGATCAGACCTCCGC 1008

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 05:10:58 ; Search time 416.945 Seconds
(without alignments)
9058.550 Million cell updates/sec

Title: US-10-023-530-3
Perforated: 1690

Sequence: 1 ccgagcgctgtgttgcgc.....ccaaaaa 1680

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 3: /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq: *
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- 11: /cgn2_6/ptodata/1/pubnpa/US09C_PUBCOMP.seq: *
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- 15: /cgn2_6/ptodata/1/pubnpa/US10_NEW_PUB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

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1	1680	100.0	1680	14	US-10-023-550-3	Sequence 3, April
2	1602.6	95.4	1692	9	US-09-821-803A-5	Sequence 5, April
3	1456.6	86.7	1873	9	US-09-821-803A-1	Sequence 1, April
4	1445.6	86.0	1664	9	US-09-821-803A-3	Sequence 3, April
5	432	25.7	432	10	US-09-796-652-5016	Sequence 5016, April
6	432	25.7	432	14	US-10-040-862-5016	Sequence 5016, April
7	415.2	24.7	640	10	US-09-879-536-636	Sequence 636, April
8	402.6	24.0	446	10	US-09-796-632-356	Sequence 636, April
9	402.6	24.0	446	14	US-10-040-862-356	Sequence 636, April
10	368.8	22.0	381	11	US-09-803-719-1629	Sequence 1629, April
11	240.2	14.3	421	10	US-09-960-352-7183	Sequence 7183, April
12	238.4	14.2	795	12	US-10-224-356-29	Sequence 29, April
13	238.4	14.2	3389	12	US-10-224-356-12	Sequence 12, April
14	238.4	14.2	3393	12	US-10-224-356-14	Sequence 14, April
15	238.4	14.1	3393	12	US-10-224-356-15	Sequence 15, April
16	236.8	14.1	3144	14	US-10-270-845-2	Sequence 2, April

C	17	123.2	7.3	465	14	US-10-198-8456-1480	Sequence 1480, App
C	18	96	5.7	355	10	US-09-960-532-9368	Sequence 9368, App
C	19	62.4	3.7	510	14	US-10-270-845-4	Sequence 4, App1
C	20	46.2	2.8	797	13	US-10-027-632-146358	Sequence 146358,
C	21	46.2	2.8	797	13	US-10-027-632-146359	Sequence 146359,
C	22	44.2	2.6	16291	12	US-10-017-161-2397	Sequence 2397, App
C	23	41.6	2.5	724	12	US-10-140-472-60	Sequence 60, App
C	24	41.6	2.5	724	12	US-10-141-761-60	Sequence 60, App
C	25	41.6	2.5	724	12	US-10-123-155-60	Sequence 60, App
C	26	41.6	2.5	724	15	US-10-146-731-60	Sequence 60, App
C	27	41	2.4	1049	12	US-10-140-472-358	Sequence 358, App
C	28	41	2.4	1049	12	US-10-141-761-358	Sequence 358, App
C	29	41	2.4	1049	14	US-10-123-155-358	Sequence 358, App
C	30	41	2.4	1049	15	US-10-146-731-358	Sequence 358, App
C	31	38.8	2.3	1431	14	US-10-156-761-7041	Sequence 7041, App
C	32	38.8	2.3	9025608	14	US-10-156-761-1	Sequence 1, App1
C	33	38.2	2.3	978	14	US-10-156-761-6381	Sequence 6381, App
C	34	38	2.3	3914	11	US-09-971-708-1	Sequence 1, App1
C	35	37.6	2.2	2631	14	US-10-156-761-6208	Sequence 6208, App
C	36	37.6	2.2	9025608	14	US-10-156-761-1	Sequence 1, App1
C	37	37.4	2.2	651	14	US-10-263-677-6	Sequence 6, App1
C	38	37.4	2.2	1143	14	US-10-263-677-6	Sequence 4, App1
C	39	37.4	2.2	1221	14	US-10-263-677-3	Sequence 3, App1
C	40	37.4	2.2	1221	14	US-10-012-542-471	Sequence 471, App
C	41	37.4	2.2	1379	14	US-10-012-542-124	Sequence 124, App
C	42	37.4	2.2	1855	13	US-10-000-512-5	Sequence 5, App1
C	43	37.4	2.2	1869	12	US-10-137-870-269	Sequence 269, App
C	44	37.4	2.2	1869	12	US-10-140-018-269	Sequence 269, App
C	45	37.4	2.2	1869	12	US-10-140-021-269	Sequence 269, App

ALIGNMENTS

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RESULT 1
US-10-023-530-3
Sequence 3, Application US/10023530
Publication No. US20030007956A1
GENERAL INFORMATION:
APPLICANT: LEGRAIN, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BIOT, Guillaume
APPLICANT: LASSOT, Irina
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TRCP
FILE REFERENCE: B471A
CURRENT APPLICATION NUMBER: US/10/023,530
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1680
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1680)
OTHER INFORMATION: Ras SFL
US-10-023-530-3

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Query Match	100.0%	Score 1680	DB 14	Length 1680
Best Local Similarity	100.0%	Pred. No.	0	
Matches 1680; Conservative	0	Mismatches	0	Gaps 0

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Db 1 CCGGGGGGAGTGTGGCGGCTAGGACGCGCCGACCTGGGGAGCGGGCGGGTACGGCTAT 60
QY 61 GGGCGGAGCGGAGAGCGCCCTTCCTTTTGAAATGACCTGGACAGCAGCAGCAGACAGTGGCTA 120
Db 61 GGGCGGAGCGGAGAGCGCCCTTCCTTTTGAAATGACCTGGAGCACACAGAGACACTGGCTA 120

121 CTGACCCAGAGAGACTCGGAGCTCGAGCTGAGTACTTTCACCCGGGACACTGCT 180
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181 AGCTGCGAGCGCGCGCGGACCAAGGAGGAGCTGTGAGTGGGAGACACTGACCTTTC 240
181 AGCTGCGAGCGCGCGCGGAGCAAGGAGGAGCTGTGAGTGGGAGACACTGACCTTTC 240
241 TCAAGCTGAGATGAGCAGAGATCAAGAGTACATATGCCAGATCAACAGCAACTTTC 300
241 TCAAGCTGAGATGAGCAGAGATCAAGAGTACATATGCCAGATCAACAGCAACTTTC 300
301 CATAGCTGTGAACAAGAGCGTCTTCTACACAGCTTATCAAGTTACAGTGAAGCTGT 360
301 CATAGCTGTGAACAAGAGCGTCTTCTACACAGCTTATCAAGTTACAGTGAAGCTGT 360
361 GCGCCCTGTCTGTGCGCTCCAGCAAGAACCAACCTCTTGGAGAGATGCGCGCGGG 420
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421 CCCAGGAGCGGGGACAAAGTGTCAAGCGCGGCACTTCTTTCCTTTCCTTTCCTTTC 480
421 CCCAGGAGCGGGGACAAAGTGTCAAGCGCGGCACTTCTTTCCTTTCCTTTCCTTTC 480
481 CAACGACCTGATGTGCTGTACAGCAGACAGGCGACGTGAATCATTTAGGCGCTGTGCG 540
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541 AAAGTTCTGTGTGTGATGATGACCCCGCAAGTTTGAAGTTCAGTGAAGCTGCA 600
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721 GAAGTGTGAGCGCTTTCAGCATGCTGAACTACATACCTTCTTACGATCTGACAGCGGA 780
721 GAAGTGTGAGCGCTTTCAGCATGCTGAACTACATACCTTCTTACGATCTGACAGCGGA 780
781 GAGAGGAGAGACCTCCGCGCAGATCTGAGAGTACTCTATTTCCGCGCAAGATGCA 840
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901 AGCAGGAGCGCCAAAGTGTGCGCTGTGAGTGTGAGAGGCGCAGTGGGCGCTGTGAAT 960
901 AGCAGGAGCGCCAAAGTGTGCGCTGTGAGTGTGAGAGGCGCAGTGGGCGCTGTGAAT 960
961 GAGTGTGATGAGAGCGCTCTGCTGTGAGGAGATGAGCCCAAGAAACAGGAAGTACT 1020
961 GAGTGTGATGAGAGCGCTCTGCTGTGAGGAGATGAGCCCAAGAAACAGGAAGTACT 1020
1021 TGCTCCCTGTGTGCTACCTATGAGGTGAGAGCAGTATGCTGTGACCCCTTGTCCCTCAT 1080
1021 TGCTCCCTGTGTGCTACCTATGAGGTGAGAGCAGTATGCTGTGACCCCTTGTCCCTCAT 1080
1081 TACTGGGCGCTTATGAGGCGCAGGCGCTGCTGAGAAGTGTCTCAGGCGCTGAGAGAGT 1140
1081 TACTGGGCGCTTATGAGGCGCAGGCGCTGCTGAGAAGTGTCTCAGGCGCTGAGAGAGT 1140
1141 GGTGCAACAGAGATCTCTCTCAATTTTGTCTCAGAAAGTGAATTTTGGAGACCTGCA 1200
1141 GGTGCAACAGAGATCTCTCTCAATTTTGTCTCAGAAAGTGAATTTTGGAGACCTGCA 1200
1201 AACGAAACAGGATGATGTTTGGAGGAGTGAAGGCGCTCATCTATGAGAGAAAGTTTGA 1260

1201 AACGAAACAGGATGATGTTTGGAGGAGTGAAGGCGCTCATCTATGAGAGAAAGTTTGA 1260
1261 TCTTGAATGTGTCTCAGATATCTCTTATCAAGCTTAAGGCTGGGTGCTCAGAAATAGGC 1320
1261 TCTTGAATGTGTCTCAGATATCTCTTATCAAGCTTAAGGCTGGGTGCTCAGAAATAGGC 1320
1321 AGGATGAGAGAGAGTGTGTGTTTCTCTCAAGTGTGCAACTCTCTCAGACCCCTGAGG 1380
1321 AGGATGAGAGAGAGTGTGTGTTTCTCTCAAGTGTGCAACTCTCTCAGACCCCTGAGG 1380
1381 TCAGGAGTGTGTGCTCAGATATGAGTGTGCTTAACTTCAATATGAGAGAGATGTC 1440
1381 TCAGGAGTGTGTGCTCAGATATGAGTGTGCTTAACTTCAATATGAGAGAGATGTC 1440
1441 CCTGGGCGCAGGCTGTGTGATGATGAGGAGCAGTGGCGCGGCTTCAATCTTATTTGCTAAT 1500
1441 CCTGGGCGCAGGCTGTGTGATGATGAGGAGCAGTGGCGCGGCTTCAATCTTATTTGCTAAT 1500
1501 CAAAGCCAGGCTCTCTCCCTCAGGATGTTTATGAAAGTGTGATGATGATGATGAT 1560
1501 CAAAGCCAGGCTCTCTCCCTCAGGATGTTTATGAAAGTGTGATGATGATGATGAT 1560
1561 GGTGCGCTCAGCTAAATGCTCTCTGTGGGAAAGGCTGTGGGAGCAGTATCATCAGG 1620
1561 GGTGCGCTCAGCTAAATGCTCTCTGTGGGAAAGGCTGTGGGAGCAGTATCATCAGG 1620
1621 CCTGGGCGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1621 CCTGGGCGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680

RESULT 2

US-09-821-803A-5
; Sequence 5, Application US/09821803A
; Patent No. US20020098530A1
; GENERAL INFORMATION:
; APPLICANT: Pfeiffer, Gerd P.
; TITLE OF INVENTION: Lung Cancer Tumor Suppressor Gene
; FILE REFERENCE: 1954-335-II
; CURRENT APPLICATION NUMBER: US/09/821,803A
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(821)
US-09-821-803A-5

Query Match 95.4%; Score 1602.6; DB 9; Length 1692;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

48 CGGCTAGGCGCTATGAGGCGGAGGCGGCGCTTCTTGAATGAACTGTGAGAGCAGCA 107
1 CGGCTAGGCGCTATGAGGCGGAGGCGGCGCTTCTTGAATGAACTGTGAGAGCAGCA 60
108 CGAGCAGTGTGCTATGAGCAGCAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 167
61 CGAGCAGTGTGCTATGAGCAGCAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 120
168 CGGCAACCTGCTATGCTGAGGCGCGCGGAGCAGAGAGCAGCAGTGTGAGTGTGAGTGTGAGT 227
121 CGGCAACCTGCTATGCTGAGGCGCGCGGAGCAGAGAGCAGCAGTGTGAGTGTGAGTGTGAGT 180
228 CAGCTGACCTTCTCAAGCTGAGTGTGAGCAGAGAGATCAAGAGTCAATGCCCCAGATCA 287

[illegible]

Query Match	86.7%: Score 1456.6; DB 9; Length 1873;	Best Local Similarity 98.9%: Pred. No. 0;	Matches 1477; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
190 GCCCGCGCGGACGACGAGCCCTGCGAGTGGAGACACCTGACCTTTCTCAAGCTGA	249		
380 GCGGGACACGAACTGGACGAGCCTGTGGATGGGAGACACCTTCTCAAGCTGA	439		
250 GATTGAGCAGAAATCAAGAGTACAAATGCCCACATCAACAGCAACCTCTTCATAGACCTT	309		
440 GATTGAGCAGAAATCAAGAGTACAAATGCCCACATCAACAGCAACCTCTTCATAGACCTT	499		
310 GAACAAGAGCGGTTCTTACACAGCCTTCATCAAGCTTCAAGCTTCAAGCTTCAAGCTT	369		
500 GAACAAGAGCGGTTCTTACACAGCCTTCATCAAGCTTCAAGCTTCAAGCTTCAAGCTT	559		
370 CTCTGTGCGCCCTCCAGCAAGAACCCCTCTTCAGAGATCCCGGGGGGGCCAGAGACG	429		
560 CTCTGTGCGCCCTCCAGCAAGAACCCCTCTTCAGAGATCCCGGGGGGGCCAGAGACG	619		
430 GCGCACAAGTGTACGCGCGCCGACCTTCCTTTTACCTGCCCAAGATCTGTCAAGACCT	489		

Dd	620	GGGCAAGAGTGTCAAGGGCCCGCACGTCTCTTTTAACTGTGCCAAAGATGCTGTCAAGCACT	679
Oy	490	GCATGTGCTGTACAGCACACAAAGGCACTGAAAGTCATTATAGGCCCTGCTGGAAAGTCTT	549
Dd	680	ACATGTGCTGTACAGCACACAAAGGCACTGAAAGTCATTATAGGCCCTGCTGGCAAAAGTCTT	739
Oy	550	GGTGGTGAATACCCCGCAGTTTGGACCTTTTGAAGGGGCTACAGCTGCACGGCCAACT	609
Dd	740	GGTGTAGATACCCCGCAAGTTTGACCTTTTGAAGGGCTGAGCTCACGGCCAAAGT	799
Oy	610	GTACTTGGGAAGCTGTGTGATGATGAGACAGCCCCCTGGGCTGGGGCTCTCGCAGGGCC	669
Dd	800	GTACTTGGGAAGCTGTGTGATGATGAGACAGCCCCCTGGGCTGGGGCTCTCGCAGGGCC	859
Oy	670	CAGTGACAAAGGCCCTGAGCTTTGTCTGTAGAAATAATGCTCTGGGAGGTGAAGTGGGA	729
Dd	860	CAGTGACAAAGGCCCTGAGCTTTGTCTGTAGAAATAATGCTCTGGGAGGTGAAGTGGGA	919
Oy	730	CGCCCTGAGCATGGCTGTGATACATTAATCTTACGTACCTGTGACAGCGGAGAGAGAGA	789
Dd	920	CGCCCTGAGCATGGCTGTGATACATTAATCTTACGTACCTGTGACAGCGGAGAGAGAGA	979
Oy	790	GCACCTCCGGCAGATTCCTGCAGAAATCTCCTAATGCCGCCAGAAAGATCCAAAGGCCCT	849
Dd	980	GCACCTCCGGCAGATTCCTGCAGAAATCTCCTAATGCCGCCAGAAAGATCCAAAGGCCCT	1039
Oy	850	GCAGCGCTGCCCTTGGGTGACCTCTTGTACCCCCAGGTGGAAGGACAGACAGAGCAG	909
Dd	1040	GCAGCGCTGCCCTTGGGTGACCTCTTGTACCCCCAGGTGGAAGGACAGACAGAGCAG	1099
Oy	910	CGCCCAAGTGGGTGCGCGTGTGATGTGACAGGGGCCAGTGGGCCCTGTGGAATGATGTGTCA	969
Dd	1100	CGCCCAAGTGGGTGCGCGTGTGATGTGACAGGGGCCAGTGGGCCCTGTGGAATGATGTGTCA	1159
Oy	970	TGGAAGGCCCTCTGTGCTGGGGGAATGAGCCAGCAAGAACAGCAGAAATGCTGTCTCCCTG	1029
Dd	1160	TGGAAGGCCCTCTGTGCTGGGGGAATGAGCCAGCAAGAACAGCAGAAATGCTGTCTCCCTG	1219
Oy	1030	TGTCCACCTAATGGGTGTAGCCAGATATGTGCTGTGACACCCCTGTGCTCATTTACTGGGCC	1089
Dd	1220	TGTCCACCTAATGGGTGTAGCCAGATATGTGCTGTGACACCCCTGTGCTCATTTACTGGGCC	1279
Oy	1090	TTAGTGGGCCAAGGGGTGCGCTGAGAAAGTGTGTCCAGCGCTGCACAGGAGTGTGTGCAGAC	1149
Dd	1280	TTAGTGGGCCAAGGGGTGCGCTGAGAAAGTGTGTCCAGCGCTGCACAGGAGTGTGTGCAGAC	1339
Oy	1150	AGAAGTCTCTCAATTTTGTCTCAGAAATGAAATCTTGGAGACCCCTGCACAAAGAAC	1209
Dd	1340	AGAAGTCTCTCAATTTTGTCTCAGAAATGAAATCTTGGAGACCCCTGCACAAAGAAC	1399
Oy	1210	GGGTCTATTTTGCAGGGGTGACGGCCCTCATCTATGAGAAAGGTTTGGATCTTGAATG	1269
Dd	1400	GGGTCTATTTTGCAGGGGTGACGGCCCTCATCTATGAGAAAGGTTTGGATCTTGAATG	1459
Oy	1270	TGTGTCTCAGGAATTCCTATATCAGAGCTTAAGGCTGGGTCTCAGAAATAGCAGGCAATTGA	1329
Dd	1460	TGTGTCTCAGGAATTCCTATATCAGAGCTTAAGGCTGGGTCTCAGAAATAGCAGGCAATTGA	1519
Oy	1330	GGAAAGAGCTTGGTTTCTCTTAAGAGTCCAACTCTCACACACCCTGAGGTCAGGGAGT	1389
Dd	1520	GGAAAGAGCTTGGTTTCTCTCTACAGTGTCCAACTCTCACACACCCTGAGGTCAGGGAGT	1579
Oy	1390	GCTGGCTCACAGTACAGCATGTGCTTAATGCTTCATATGAGAGGATGTCTCTGGGCCA	1449
Dd	1580	GCTGGCTCACAGTACAGCATGTGCTTAATGCTTCATATGAGAGGATGTCTCTGGGCCA	1639
Oy	1450	GGGTCTGTGTAAATGTGGGCACTGGCCAGGTTCAATACCTAATTTGCTAATCAAAAGCCAG	1509
Dd	1640	GGGTCTGTGTAAATGTGGGCACTGGCCAGGTTCAATACCTAATTTGCTAATCAAAAGCCAG	1699
Oy	1510	GGTCTCTCCCAAGGTGTTTTTAAAGATCGTGAATGTATGTAAATGTGTGGTGGCTC	1569
Dd	1700	GGTCTCTCCCAAGGTGTTTTTAAAGATCGTGAATGTATGTAAATGTGTGGTGGCTC	1759

Db	1760	AGCTGAATGCTCTCTGTGGGAAAAGGGGTTGGGTGAGACATCATCAGG--CCTGGGG	1627
Qy	1570	AGCTGAATGCTCTCTGTGGGAAAAGGGGTTGGGTGAGACATCATCAGG--CCTGGGG	1627
Qy	1570	AGCTGAATGCTCTCTGTGGGAAAAGGGGTTGGGTGAGACATCATCAGG--CCTGGGG	1627
Db	1760	AGCTGAATGCTCTCTGTGGGAAAAGGGGTTGGGTGAGACATCATCAGGCGCTGGGGC	1819
Qy	1528	CTGAGAGAAATTGGCTCAATAAAGATTTCAGATCCAAAAAATTTTTTTTTT	1680
Db	1820	CTGAGAGAAATTGGCTCAATAAAGATTTCAGATCCAAAAAATTTTTTTTTT	1872
RESULT 4			
US-09-821-803A-3			
Sequence 3, Application US/09821803A			
Patent No. US20020098530A1			
GENERAL INFORMATION:			
APPLICANT: Pelfer, Gerd P.			
TITLE OF INVENTION: Lung Cancer Tumor Suppressor Gene			
FILE REFERENCE: 1954-335-II			
CURRENT APPLICATION NUMBER: US/09/821,803A			
CURRENT FILING DATE: 2001-03-30			
PRIOR APPLICATION NUMBER: US 60/193,268			
PRIOR FILING DATE: 2000-03-30			
NUMBER OF SEQ ID NOS: 19			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 3			
LENGTH: 1664			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (282)..(848)			
US-09-821-803A-3			
Query Match			
Best Local Similarity 86.0% Score 1445.6; DB 9; Length 1664;			
Matches 1477; Conservative 0; Mismatches 14; Indels 3; Gaps 2;			
Qy	190	GCCGCGCCGGGAGCCAGCAGACGCTGTGGAGTGGGAGACACCTGACCTTCTCAAGCTGA	249
Db	170	GCGGAGACAGAAAGCGAGAGCGCTGTGGAGTGGGAGACACCTGACCTTCTCAAGCTGA	229
Qy	250	GATTGAGCAGAAATCAAGAAGTACATGCCAGATCCCAAGTCAACAGCAACCTTTATGAGCTT	309
Db	230	GATTGAGCAGAAATCAAGAAGTACATGCCAGATCCCAAGTCAACAGCAACCTTTATGAGCTT	289
Qy	310	GAACAAGAGCGTCTTACACAGGCTTCATCAAGTTAGCTGAAGCTGGGGCCCTCT	369
Db	290	GAACAAGAGCGTCTTACACAGGCTTCATCAAGTTAGCTGAAGCTGGGGCCCTCT	349
Qy	370	CTCTGTGCCCTTCACAGCAAGAAGCCACCTCTTCAGAGATCCCGCGGGGCCACAGAGC	429
Db	350	CTCTGTGCCCTTCACAGCAAGAAGCCACCTCTTCAGAGATCCCGCGGGGCCACAGAGC	409
Qy	430	GGGCAACAAGTTCACAGGCGCGCACTTCCTTTACCTGCGCAAGATGCTTCAGACACT	489
Db	410	GGGCAACAAGTTCACAGGCGCGCACTTCCTTTACCTGCGCAAGATGCTTCAGACACT	469
Qy	490	GCATGTGCTGCACAGCAAGGGGACGTGAAGTCAATGAGGCCCTGCTGGCAAAAGTTCTT	549
Db	470	GCATGTGCTGCACAGCAAGGGGACGTGAAGTCAATGAGGCCCTGCTGGCAAAAGTTCTT	529
Qy	550	GGTGGTGAATACCCCGCAAGTTTGCACTTTTGAGCGGCTGAGCTACAGGCCAAGT	609
Db	530	GGTGGTGAATACCCCGCAAGTTTGCACTTTTGAGCGGCTGAGCTACAGGCCAAGT	589
Qy	610	GTACTTGGGAGCTGTGTGATGATGACAGACCCCTGCGGGCTCTGCGAGGGCC	669
Db	590	GTACTTGGGAGCTGTGTGATGATGACAGACCCCTGCGGGCTCTGCGAGGGCC	649
Qy	670	CAGTGACAAGGCCCTGAGCTTTGTCCTGAAGAAATGATCTTGGGAGAGTGAACTGGGA	729
Db	650	CAGTGACAAGGCCCTGAGCTTTGTCCTGAAGAAATGATCTTGGGAGAGTGAACTGGGA	709


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OY 730 GCCTTCAGCATGCTGTGACATACATACCTTCTTACGTATCTTCAGCGGAGAGAGAGA 789
DB 710 GCCTTCAGCATGCTGTGACATACATACCTTCTTACGTATCTTCAGCGGAGAGAGAGA 769
OY 790 GCACCTCCGGCAGATCTTCAGCAAGATACCTTCTTATGCGCCAGAAAGATCCAGAGCCCT 849
DB 770 GCACCTCCGGCAGATCTTCAGCAAGATACCTTCTTATGCGCCAGAAAGATCCAGAGCCCT 829
OY 850 GCACGCTGCCCCCTTGGGTGACCTTGTATACCCCGAGTGGAGGAGAGAGAGAGAGAG 909
DB 830 GCACGCTGCCCCCTTGGGTGACCTTGTATACCCCGAGTGGAGGAGAGAGAGAGAGAG 889
OY 910 GCACGAGTGCCTGCGGTGTGATGTACAGGCGCAGTGGGCGCTTGTGAATGATGTGCA 969
DB 890 GCACGAGTGCCTGCGGTGTGATGTACAGGCGCAGTGGGCGCTTGTGAATGATGTGCA 949
OY 970 TGGAGGCCCCCTTCTGTGCTGTGGGGATGTAGCCAGCAAGAGAGAGAGAGAGAGAG 1029
DB 950 TGGAGGCCCCCTTCTGTGCTGTGGGGATGTAGCCAGCAAGAGAGAGAGAGAGAGAG 1009
OY 1030 TGTCCACCTATGAGGTGTAGCCAGTATGAGCTGTGACCCCTGTGCGCTCATCTAGTGGCC 1089
DB 1010 TGTCCACCTATGAGGTGTAGCCAGTATGAGCTGTGACCCCTGTGCGCTCATCTAGTGGCC 1069
OY 1090 TTAGTGGCCAGAGGCTGCTGTGAGAACTGTCTCAGGCGCTGAGAGAGAGAGAGAGAG 1149
DB 1070 TTAGTGGCCAGAGGCTGCTGTGAGAACTGTCTCAGGCGCTGAGAGAGAGAGAGAGAG 1129
OY 1150 AGAATCTCTCTCAATTTTGTCTCAGAAAGTGAATACTTGGAGAGAGAGAGAGAGAGAG 1209
DB 1130 AGAATCTCTCTCAATTTTGTCTCAGAAAGTGAATACTTGGAGAGAGAGAGAGAGAGAG 1189
OY 1210 GGGTCATGTTTGCAGAGGAGTGAAGGCGCTCATCTATGAGAAAGTGGTGGATCTTGAATG 1269
DB 1190 GGGTCATGTTTGCAGAGGAGTGAAGGCGCTCATCTATGAGAAAGTGGTGGATCTTGAATG 1249
OY 1270 TGGTCTCAGGATATCTTATCAGAGCTTAAGGCTGAGTGTGCTCAGAAATAGCAGGCAATGA 1329
DB 1250 TGGTCTCAGGATATCTTATCAGAGCTTAAGGCTGAGTGTGCTCAGAAATAGCAGGCAATGA 1309
OY 1330 GGAAGAGCTTGTGCTCTCTCAGAGTGCACACCTCTCAGACACCTTGAGTGCAGAGAGT 1389
DB 1310 GGAAGAGCTTGTGCTCTCTCAGAGTGCACACCTCTCAGACACCTTGAGTGCAGAGAGT 1369
OY 1390 GCTGCTCAGATACAGATGATGCTTATGCTTATGAGAGAGATGCTCTGGGCA 1449
DB 1370 GCTGCTCAGATACAGATGATGCTTATGCTTATGAGAGAGATGCTCTGGGCA 1429
OY 1450 GGGTCTGTGTGATGTGGGCACTGGCCAGGTTTCAATCTTATTTGCTATCAGAAAGCCAG 1509
DB 1430 GGGTCTGTGTGATGTGGGCACTGGCCAGGTTTCAATCTTATTTGCTATCAGAAAGCCAG 1489
OY 1510 GGTCTCTCTCTCAGAGTGTGTTTATGAGAGTGCAGTATGATGATGTGTGTGGCT 1568
DB 1490 GGTCTCTCTCTCAGAGTGTGTTTATGAGAGTGCAGTATGATGATGTGTGTGGCT 1549
OY 1569 CAGCTGAAGTCTCTGTGTGGGAAAGGGGTTGGGTTGACAGTCAATCATCAGG - CCGTGGG 1626
DB 1550 CAGCTGAAGTCTCTGTGTGGGAAAGGGGTTGGGTTGACAGTCAATCATCAGG - CCGTGGG 1609
OY 1637 GCTGAGAGATGCTCTCAATAAAGATTTCAAGATCCAAAGAGAGAGAGAGAGAGAG 1680
DB 1610 CCGTGAAGAAATGCTGTCAATTAAGATTTCAAGATCTCTCAAGAGAGAGAGAGAGAGAG 1663

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RESULT 5

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US-09-796-692-5016/c
; Sequence 5016, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Galiger, Alexander
; APPLICANT: Algate, Paul A.

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; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077, 001200
; CURRENT APPLICATION NUMBER: US/09/796, 692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186, 126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190, 479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200, 545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200, 303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200, 779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200, 999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202, 084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206, 201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218, 950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222, 903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223, 416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223, 378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5016
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-5016

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Query Match 25.7%; Score 432; DB 10; Length 432;
Best local similarity 100.0%; Pred. No. 2,6e-125; Indels 0; Gaps 0;
Matches 432; Conservative 0; Mismatches 0;

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OY 1140 TGGTGCAGACAGAGTCTCTCAATTTTGTCTCAGAAAGTGAATACTTGGAGAGCCCTGC 1199
DB 432 TGGTGCAGACAGAGTCTCTCAATTTTGTCTCAGAAAGTGAATACTTGGAGAGCCCTGC 373
OY 1200 AAACAGAACAGGCTATGTTTGCAGAGGAGGAGGCGCTCATCTATGAGAGAAAGTTTGG 1259
DB 372 AAACAGAACAGGCTATGTTTGCAGAGGAGGAGGCGCTCATCTATGAGAGAAAGTTTGG 313
OY 1260 ATCTGGAATGTGTCTCAGATATCTTATCAGAGCTAAGGAGGAGGAGGAGGAGGAGG 1319
DB 312 ATCTGGAATGTGTCTCAGATATCTTATCAGAGCTAAGGAGGAGGAGGAGGAGGAGGAGG 253
OY 1320 CAGGAGTGTGAGAGAGTGTGTTTCTCTACAGTGCACACTCTCTCAGACACCTGTAG 1379
DB 252 CAGGAGTGTGAGAGAGTGTGTTTCTCTCTACAGTGCACACTCTCTCAGACACCTGTAG 193
OY 1380 GTGAGGAGTGTGCTGCTCAGATACAGCATGTGCTTATGCTTATGAGAGAGATGT 1439
DB 192 GTGAGGAGTGTGCTGCTCAGATACAGCATGTGCTTATGCTTATGAGAGAGATGT 133
OY 1440 CCTGAGGAGGAGTGTGAGATGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1499
DB 132 CCTGAGGAGGAGTGTGAGATGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 73
OY 1500 TCAGAGCAGAGGAGTGTCTCTCAGAGTGTGTTTATGAGAGTGTGAGATGTATGATGTG 1559
DB 72 TCAGAGCAGAGGAGTGTCTCTCAGAGTGTGTTTATGAGAGTGTGAGATGTATGATGTG 13
OY 1560 TGGTGGCTCAG 1571
DB 12 TGGTGGCTCAG 1

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RESULT 6
US-10-040-862-5016/C
; Sequence 5016, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5016
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-5016

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Query Match	25.7%	Score 432	DB 14	Length 432
Best Local Similarity	100.0%	Pred. No. 2,6e-125		
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Db	432	TGTGTGACAGACAGAAAGTCTCTCAATATTTTGTCTCAGAAAGTAAAAATCTTGGAGACCTGC	373	
QY	1200	AAACAGAACAGGTCATGCTTTGTCAGAGGGGTACGGCCCTCATCTATGAGGAAAGGTTTGG	1255	
Db	372	AAACAGAACAGGTCATGCTTTGTCAGAGGGGTACGGCCCTCATCTATGAGGAAAGGTTTGG	313	
QY	1260	ATCTTGAATGTGTCCTCAGATATTCCTTATAGAGCTPAAAGGGTGGCTCTCAGAAATAGG	1319	
Db	312	ATCTTGAATGTGTCCTCAGATATTCCTTATAGAGCTPAAAGGGTGGCTCTCAGAAATAGG	253	
QY	1320	CAGGCATTGAGGAAGAGTCTTGTTCTCTCTACAGTGCACACTCTTCACACACCCGTAG	1379	
Db	252	CAGGCATTGAGGAAGAGTCTTGTTCTCTCTACAGTGCACACTCTTCACACACCCGTAG	193	
QY	1380	GTCAGGAGTCTCTGGCTCACAGTACAGCATGTGCCTTAATGCTTTCATATGAGAGAGATGT	1439	

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Db      132  GTCAGGAGTGTGCTCAGCTACAGATGAGCATGTGGCTTATGCTTATATGAGGAGAGTGT 133
QY      1440  CCCTGGGCGCAGGGTGTGTGTGTAATGTGGGCACTGGCCCAAGTTCATPACCTTATTTGGCTPA 1499
Db      132  CCTTGGGCGCAGGGTGTGTGTGTAATGTGGGCACTGGCCCAAGTTCATPACCTTATTTGGCTPA 73
QY      1500  TCAAGCCAGGGTCTCTCCCTCAGGTGTTTTTATGAATGGCGTAATGTATGTAATGTG 1555
Db      72  TCAAGCCAGGGTCTCTCTCCCTCAGGTGTTTTTATGAATGGCGTAATGTATGTAATGTG 13
QY      1560  TGTGGGCTCAG 1571
Db      12  TGTGGGCTCAG 1

RESULT 7
US-09-879-536-636
; Sequence 636, Application US/09879536
; Patent No. US20020144298A1
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/879.536
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/008,801
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 636
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(640)
; OTHER INFORMATION: n = A,T,C or G
US-09-879-536-636

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	Query Match	24.7%	Score 415.2	DB 10	Length 640	
	Best Local Similarity	94.8%	Pred. M.6.1e-120			
	Matches 437	Conservative	0	Mismatches 23	Indels 1	Gaps 1
QY	941	GCCAGTGGGGCCTGTGGAATGAGTGTGCATGAGAGCCCTCCCTGTGCTGGGGAAATGACC	1000			
DB	13	GCCAGTGGGGCCTGTGGAATGAGTGTGCATGAGAGCCCTCCCTGTGCTGGGGAAATGACC	72			
QY	1001	CAGAGAACGCGAAGTAGCTTGCTCCGTGTCCACTTAATGGGTAGCCAGTATGGCT	1060			
DB	73	CAGAGAACGCGAAGTAGCTTGCTCCGTGTCCACTTAATGGGTAGCCAGTATGGCT	132			
QY	1061	CTGCACCCCTCTGGCCCTCATTAACGTGGGGCCTAATGGGGCAGGGCTGCCCTCAGAACTGCG	1120			
DB	133	CTGCACCCCTCTGGCCCTCATTAACGTGGGGCCTAATGGGGCAGGGCTGCCCTCAGAACTGCG	192			
QY	1121	TCCAGAGCCTGCAGCAGAGAGTGGTGCAGACAGAACTCTCTCAATTTTGTCTCAGAAAGTG	1180			
DB	193	TCCAGAGCCTGCAGCAGAGAGTGGTGCAGACAGAACTCTCTCAATTTTGTCTCAGAAAGTG	252			
QY	1181	AAAAATCTTGAGACCCCTGCAGAAACAGAAACAGGGTCAATGTTTGCAGGGGTGACGGCCCTCAT	1240			

Db 253 AAAATCTTGAACCCGCAACAGACAGGGCTCATGTTTCAGGGGTGACGCCCTCAT 312
Qy 1241 CATGAGGAAGAGTTTGGATCTTGATGTGCTCAGAGATACCTTATCAGAGCTAAG 1300
Db 313 CATGAGGAAGAGTTTGGATCTTGATGTGCTCAGAGATACCTTATCAGAGCTAAG 372
Qy 1301 GTGGGTGCTCAGATTAAGGACGCA-TTGAGAGAGAGTCTTGTTCTCTACAGTGCC 1359
Db 373 GTGGGTGCTCAGATTAAGGACGCAATTTGANGAAAAATCTTGAGTTCTCTTACAGTGCC 432
Qy 1360 AACTCTGACACACCGCTGAGGAGTGGTGGTCCACA 1400
Db 433 CACTTCTTACACACCCCTTGAGGAGAAATGCTGCTTACA 473

RESULT 8
US-09-796-692-3636/c
; Sequence 3636, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Galiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3636
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (409)
; OTHER INFORMATION: n-A,T,C or G
; US-09-796-692-3636

Query Match 24.0%; Score 402.6; DB 10; Length 446;
Best Local Similarity 97.6%; Pred. No. 4,7e-116;
Matches 408; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 709 CTCGTGGGAGTGAATGGAGCGCTTCAGATGCTGAACATACACTCTCTAGCTAT 768
Db 418 CTTTGGCCNTGTGAGTGGAGCGCTTCAGATGCTGAACATACACTCTCTAGCTAT 359
Qy 769 CCTGACGGGAGAGGAGAGACCTCCGCAAGATCTTGACGAAGTACTCTATTGGCG 828

Db 358 CCTGACGGGAGAGAGAGACACCTCCGCCAGATCTGACGAAGTACTCTATTGGCG 299
Qy 829 CCAGAGATCCAAAGAGGCCCTGACAGCCCTGCCCCCTGGGTGACCTCTTACCCCCAG 888
Db 298 CCAGAGATCCAAAGAGGCCCTGACAGCCCTGCCCCCTGGGTGACCTCTTACCCCCAG 239
Qy 889 TGAAGGACAGACAGCAGGAGGCCCAAGTGCCTGCGTGTGAGTGTGACAGGAGCCAGTGG 948
Db 238 TGAAGGACAGACAGCAGGAGGCCCAAGTGCCTGCGTGTGAGTGTGACAGGAGCCAGTGG 179
Qy 949 GGCCTGTGGAATGAGTGTGCATGAGAGCCCTCTGCTGTGGGGGAATGAGCCAGAGAAC 1008
Db 178 GGCCTGTGGAATGAGTGTGCATGAGAGCCCTCTGCTGTGGGGGAATGAGCCAGAGAAC 119
Qy 1009 AGCGAAGTAGCTTGCCTCCCTGTGTCCACCTATGGGTGTAGCCAGTATGGCTGTACACC 1068
Db 118 AGCGAAGTAGCTTGCCTCCCTGTGTCCACCTATGGGTGTAGCCAGTATGGCTGTACACC 59
Qy 1069 CTCGTGCCCTCATTTACTGGGCTTGTAGTGGGCCAGGCGCTGCCTGAGAACCTGTCCAGG 1126
Db 58 CTCGTGCCCTCATTTACTGGGCTTGTAGTGGGCCAGGCGCTGCCTGAGAACCTGTCCAGG 1

RESULT 9
US-10-040-862-3636/c
; Sequence 3636, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3636
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure

LOCATION: (409)
OTHER INFORMATION: n-A,T,C or G
US-10-040-862-3636

Query Match 24.08; Score 402.6; DB 14; Length 446;
Best Local Similarity 97.6%; Pred. No. 4,7e-116;
Matches 408; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 709 CTCTGGGAGCTGAGTGGGAGCGCTTCAGCATGCTGAAGTACATTAATCTCTACGAT 768
DB 418 CTTTGGCCCTMTTGCAGTGGGAGCGCTTCAGCATGCTGAAGTACATTAATCTCTACGAT 359
QY 769 CCTCAGCGGAG 828
DB 358 CTTGACCGGAG 299
QY 829 CCAGAGATCCAG 888
DB 298 CCAGAGATCCAG 239
QY 889 TGAAGGAG 948
DB 238 TGAAGGAG 179
QY 949 GGCCTGTGAGATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
DB 178 GGCCTGTGAGATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 119
QY 1009 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
DB 118 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 59
QY 1069 CTCTGCCCTCATTAATGAG 1126
DB 58 CTCTGCCCTCATTAATGAG 1

RESULT 10

US-09-803-719-1629
Sequence 1629, Application US/09803719
Publication No. US20030044783A1
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Imils, Michael A.
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Gliese, Klaus
APPLICANT: Randerzo, Filippo
APPLICANT: Kennedy, Giulia C.
APPLICANT: Pot, David
APPLICANT: Kassam, Altaf
APPLICANT: Lamson, George
APPLICANT: Drmanac, Radjoje
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana
APPLICANT: Labat, Ivan
APPLICANT: Leeshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIORITY APPLICATION NUMBER: 60/186,609
PRIORITY FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1629

LENGTH: 381
TYPE: DNA
ORGANISM: Homo sapiens
US-09-803-719-1629

Query Match 22.08; Score 368.8; DB 11; Length 381;
Best Local Similarity 99.5%; Pred. No. 1.9e-105;
Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 848 CTGCAGCCCTGCCCCCTTGGGTGACCTCTTGTACCCCGAGGTGAGAGAGAGAGAGAGAG 907
DB 10 CGGCAGCCCTGCCCCCTTGGGTGACCTCTTGTACCCCGAGGTGAGAGAGAGAGAGAGAG 69
QY 908 AGCCCAAGTGCCTGCGGTGTGAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
DB 70 AGCCCAAGTGCCTGCGGTGTGAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
QY 968 CATGAGAGCCCTCTGT 1027
DB 130 CATGAGAGCCCTCTGT 189
QY 1028 TGTGTCCACCTATGAGGTGTGAGCCAGATGAGCTGTGACCCCTGTGCTCATTAATGAGG 1087
DB 190 TGTGTCCACCTATGAGGTGTGAGCCAGATGAGCTGTGACCCCTGTGCTCATTAATGAGG 249
QY 1088 CTTATGTGAGGAG 1147
DB 250 CTTATGTGAGGAG 309
QY 1148 ACAGAACTCTCTCAATTTTGTCTCAAGAAATGTAATTTTGTGAGAGAGAGAGAGAGAG 1207
DB 310 ACAGAACTCTCTCAATTTTGTCTCAAGAAATGTAATTTTGTGAGAGAGAGAGAGAGAG 369
QY 1208 CAGGCTCATGTT 1219
DB 370 CAGGCTCATGTT 381

RESULT 11

US-09-960-352-7183
Sequence 7183, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengding
APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Nagappa
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(1029)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7183
LENGTH: 421
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 31-LIB3057-014-Q1-K1-H11
US-09-960-352-7183

Query Match 14.38; Score 240.2; DB 10; Length 421;
Best Local Similarity 86.6%; Pred. No. 5.9e-65;
Matches 290; Conservative 0; Mismatches 38; Indels 7; Gaps 2;

QY 3 GGGCGGTGTGTGAGGCTACGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 61
DB 87 GGGCGGTGTGTGAGGCTACGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 146
QY 62 GGGCGAGCGGAGG-----CGCCTTCTTGTGAATGACTGTGAGAGAGAGAGAGAGAGAGAG 115
DB 147 GGTGAGCGGAG 206
QY 116 GGTACTGACAGCAG 175

Db 1014 AGRAGTATGACAAAGTTTAGGCGAGAACTGGAGGAGCCCTT 1053

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